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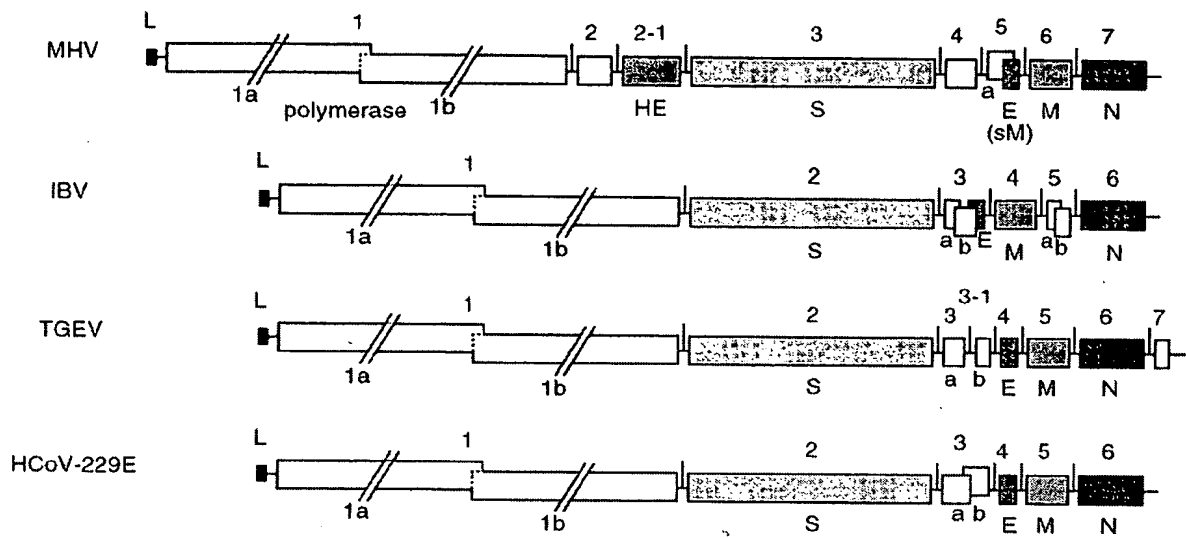
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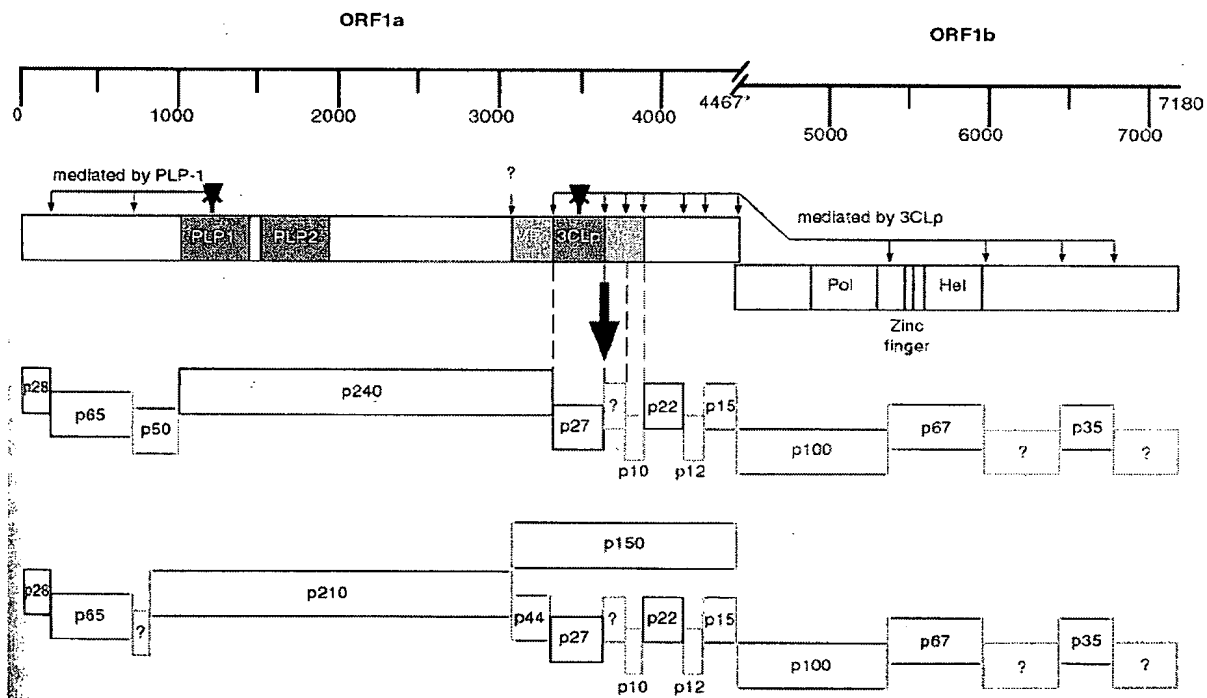
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**FIGURE 1**



**FIGURE 2**



**FIGURE 3****FIGURE 3A**

		Section 1				
		(1)	1	10	20	30 43
BCV N		(1)	ATGTCTTTT	ACTCCTGGT	-AAGCAAT-	-CCAGTAGTAGAGCGT
MHV N		(1)	ATGTCTTTT	GTTCCTGGG	CAAGAAAA	TGCCGGTGGCAGAAGCT
Avian infectious bronchitis N		(1)	-----	-----	-----	-----
Consensus		(1)	ATGTCTTTT	TCCTGG	AAG AA	CC GT G AGA T
		Section 2				
		(44)	44	50	60	70 86
BCV N		(41)	CCTTTGGAAAT	CGTTCTGGT	AATGGCATCCTTAAG	-----
MHV N		(44)	CCTCTGTAAACCG	CGCTGGTAA	TGGAATCCTCAAGAAGACCAC	
Avian infectious bronchitis N		(1)	-----	-----	-----	-----
Consensus		(44)	CCT TG AAA CG	CTGGTAATGG	ATCCT AAG	
		Section 3				
		(87)	87	100	110	129
BCV N		(76)	-TGGGCGGATCAGTCCGACCAATCTAGAAATGTTCAAACCAGG			
MHV N		(87)	TTGGGCTGACCAAAACCGAGCGTGGACCAATAATCAAAATAGA			
Avian infectious bronchitis N		(1)	-----	-ATGGCGAGCGGTAAAGCAGCTGGAAAGTCAAG		
Consensus		(87)	TGGGC GA CA	CCGAGCG T	AAGAAAT TCAAA CAGA	
		Section 4				
		(130)	130	140	150	160 172
BCV N		(118)	GGTAGAAGAGCTCAACCCCAAGCAAACCTGCTACTTCTCAGCTAC			
MHV N		(130)	GGCAGAAGGAATCAGCCAAAGCAGACTGCAACTACTCAAC--C			
Avian infectious bronchitis N		(33)	CTCCCCCGCGCCAATC--ATCAAACTAGGAGGACCAAAA--C			
Consensus		(130)	GGCAGAAG GCTCA CC	AAGCAAACCTGC	ACTACTCAAC C	
		Section 5				
		(173)	173	180	190	200 215
BCV N		(161)	CATCAGGAGCGGAATGTTGTAGCGGTACTAT-TCTTGTTTCTCTG			
MHV N		(171)	CAACTCC-GGGAGTGTGGTTCCCATTTAG-TCTTGTTTCTCTG			
Avian infectious bronchitis N		(71)	CACCAAA-GGTAGGGTCATCTGGAAATGCATCTTGTTTCAAG			
Consensus		(173)	CA CA	GGGAGTGT GT	CCC A TAC TCTTGTTTCTCTG	
		Section 6				
		(216)	216	230	240	258
BCV N		(203)	GAATTA---CTCAGTTTCAAAAAGGAAAGGAGTTTGAATTTGC			
MHV N		(212)	GCATTA---CCCAGTTCCAAAAGGAAAGGAGTTTCAAGTTTGC			
Avian infectious bronchitis N		(113)	CCATAAAGGCCAAGAACTAAATGCACCTGCACCTAAGTTTG-			
Consensus		(216)	GCATTA	CCCAGTT CAAA	GGAAAGGAGTTT	AGTTTGC
		Section 7				
		(259)	259	270	280	290 301
BCV N		(243)	AGAGCGACAAGGTGTGCCTATTGCACCAGGAGTCCCAGCTACT			
MHV N		(252)	AGAAAGGACAAGGAGTGCCTATTGCCAATGGAATCCCAGCTTCA			
Avian infectious bronchitis N		(155)	--AAGGTAGTGGTGTTCCTGATAATGAAAATCTTAAAAATAGC			
Consensus		(259)	AGAAGGACAAGGTGTGCCTATTGC	AAGGA	TCCCAGCTAC	

**FIGURE 3A (contd.)**

Section 8					
	(302)	302	310	320	330 344
BCV N	(286)	GAAGCTAAGGGGTACTGGTACAGACACAACAGAGGTTCTTTTA			
MHV N	(295)	GAGCAAAAGGGATATTGGTATAGACACAACCGCCGTTCTTTTA			
Avian infectious bronchitis N	(196)	CAGCAGCACGGGTACTGGAGGCGCCAAGCCAG-----GTTTA			
Consensus	(302)	GAGCA AAGGGGTACTGGTA AGACACAACAG CGTTCTTTTA			
Section 9					
	(345)	345	350	360	370 387
BCV N	(329)	AAACAGCCGATGGCA-ACCAGCGTCAACTGCTGCCACGATGGT			
MHV N	(338)	AAACACCTGATGGGC-AGCAGAAAGCAATTACTGCCCAGATGGT			
Avian infectious bronchitis N	(233)	AGCCAGGTAAAGGCGGAAGAAAACCAAGTCCCTGATGCC-TGGT			
Consensus	(345)	AAACAGCTGATGGC A CAGAA CAATT CTGCC CGATGGT			
Section 10					
	(388)	388	400	410	420 430
BCV N	(371)	ATTTTACTATCTTGGAAACAGGACCGCATGCCAAGAGCCAGTA			
MHV N	(380)	ATTTTACTATCTTGGCACAGGGGCCCATGCTGGAGCCAGTTA			
Avian infectious bronchitis N	(275)	ATTTCTATTACACTGGAACAGGACCCAGCCCTGACCTGAATTG			
Consensus	(388)	ATTTTACTATCTTGGAAACAGGACC CATGCTGAAG CAATTA			
Section 11					
	(431)	431	440	450	460 473
BCV N	(414)	TGGCACCGATATTGACGGAGTCTCTGGGTCGCTAGTAACCCAG			
MHV N	(423)	TGGAGACAGCAATTGAAGGTGCTCTCTGGGTTGCCAAGAGCCAA			
Avian infectious bronchitis N	(318)	GGGTGATTCTCAAGATGGGTATAGTGTGGGTTGGCTGAAGGGT			
Consensus	(431)	TGG GAC TATTGA GGTGTCTTCTGGGTTGCTA TAACCA			
Section 12					
	(474)	474	480	490	500 516
BCV N	(457)	GCTGATGTCAATAACCCGGCTGACATTCTCGATCGGGACCCAA			
MHV N	(466)	GCGGACACCAATAACCGCTCTGATATTGTGGAAGGAGCCAA			
Avian infectious bronchitis N	(361)	GCTGATGTGAAATCTAGATCCAAACAGGGTACTAGAGATCCTG			
Consensus	(474)	GCTGATGTCAATAACCCG TCTGACATTGTGATAGGGACCCAA			
Section 13					
	(517)	517	530	540	559
BCV N	(500)	GTAGCGATGAGGCTATTCCGACTA-GGTTTCCGCTGGCAGCG			
MHV N	(509)	GCAGTCATGAGGCTATTCTACTA-GGTTTGCGCCGGCAGCG			
Avian infectious bronchitis N	(404)	ATAAGTTTGAT-CAATACCCACTACGGTTTTCAGATGG-----			
Consensus	(517)	GTAG ATGAGGCTATTCC ACTA GGTTT CGCCTGGCAGCG			
Section 14					
	(560)	560	570	580	590 602
BCV N	(542)	TACTCCCTCAGGGTTACTATATTGAAGGCTCAGGAAGGTCTGC			
MHV N	(551)	TATTGCCCTCAGGGCTTTTATGTTGAAGGCTCTGGAAGGTCTGC			
Avian infectious bronchitis N	(441)	-AGGACCTGATGGTAATT-----TCCGTTGGGACTTTC			
Consensus	(560)	TA T CCTCAGGGTTATTAT TTGAAGGCTC GGAAGGTCTGC			



**FIGURE 3A (contd.)**

Section 15					
	(603)	603	610	620	630 645
BCV N	(585)	TCCTAATTCCAGATCTACTTCACGCGCA - - TCCAGTAGAGCC			
MHV N	(594)	ACCTGCTAGCCGATCTGTTTCGCGGT CACAATCCCGTGG - GCC			
Avian infectious bronchitis N	(472)	AT - TCCTCTGAGTCGTGGTAGGAGTGGGAAGATCAACCGCAGCA			
Consensus	(603)	ACCT CT	CAGATCTGGTTCGCG	GCA	ATCCAGTGGAGCC
Section 16					
	(646)	646	660	670	688
BCV N	(625)	TCTAGTGCAAGGATCGCGTAGTAGAGCCCAATTCTGGCAACAGAA			
MHV N	(636)	AAATA - - - - - ATCGCG - - CTAGAAGCAGTTC CAACAGCGCC			
Avian infectious bronchitis N	(514)	TCATCAGCGGCATCTAG - - - TAGAGTACCATCCCGTGAGGGTT			
Consensus	(646)	TCAT	GC G ATCGCG	TAGAG CA	TTCC GC AG G
Section 17					
	(689)	689	700	710	720 731
BCV N	(668)	CCCCTACCTCTGGTGTACAGCTGATATGGCTGATCAAATTGC			
MHV N	(671)	AGCCTGCCCTCTACTGTAAAAGCTGATATGGCCGAAGAAATTGC			
Avian infectious bronchitis N	(554)	CAGCTGGTCTGTAGGAGTGGAGCTGA - - - AGATGATCTGATTGC			
Consensus	(689)	C	CCTGCCTCTAGTGTA	ACCTGATATGGCTGATCAAATTGC	
Section 18					
	(732)	732	740	750	760 774
BCV N	(711)	TAGTCTTCTTCTGGCAAAACCTGGCAAGGATGGCACTAAGGCCA			
MHV N	(714)	TGCTCTTGTTTTGGCTAAGCTCGGTAAAGATGGCGGCCAGGCC			
Avian infectious bronchitis N	(594)	CCGTGCAGCAAAGATTATTCAGGAGCAGCAG - - - AGGAAGGGT			
Consensus	(732)	T	GTCTTGTT	TGGCTAA CT	GGCAAGGATGCCAG AAGCC
Section 19					
	(775)	775	780	790	800 817
BCV N	(754)	CAGCAAGTAACCTAAGCAGACTGCCAAAGAAATCAGACA - - GAA			
MHV N	(757)	AAGCAAGTAACGAAGCAAGTCCCAAAGAGTCAGGCA - - GAA			
Avian infectious bronchitis N	(634)	ACGCGCATTACTAAGCANAAGGCAGAAAGAGATGGCTCATCGCC			
Consensus	(775)	AAGCAAGTAACCTAAGCAA	TGCCAAAGAAATCAG	CA	GAA
Section 20					
	(818)	818	830	840	850 860
BCV N	(795)	AATTTTGAATAAGCCCCGCCAGAAAGAGGAGCCCCAATAAACA			
MHV N	(798)	AATTTTAAACAAGCCTCGGCCAAAGAGGACTCCAAACAAGCAG			
Avian infectious bronchitis N	(677)	GATTCGTAAAGCGTACGGTGCCACCAGGTTATAGAGTAGATCA			
Consensus	(818)	AATTTTGA	AAGCCCCGCCA	AAGAGGA	CC AATAAACA
Section 21					
	(861)	861	870	880	890 903
BCV N	(838)	TGCACGTGTCAGCAGTGTTTTGGGAAGAGAGGCCCCCAATCAGA			
MHV N	(841)	TGCCAGTGCAGCAGTGTTTTGGAAAGAGAGGCCCCCAATCAGA			
Avian infectious bronchitis N	(720)	AGTTTTTGGCCCTCGTACTAAAGCTAAAGAGGGT - - - - - A			
Consensus	(861)	TGC	CTGTGCAGCAGTGT	TTTTTGGGAAGAGAGGCCCCCAATCAGA	

**FIGURE 3A (contd.)**

Section 22							
	(904)	904	910	920	930	946	
BCV N	(881)	ATTTTGGTGGTGGAGAAATGTTAAAACTTGGAACTAGTGACCC					
MHV N	(884)	ATTTTGGAGGCTCTGAAATGTTAAAACTTGGAACTAGTGATCC					
Avian infectious bronchitis N	(755)	ATTTTGGTGATGACAAGATGAATGAGGAAGGTATTAAGGATGG					
Consensus	(904)	ATTTTGGTGGTG	GAAATGTTAAAACTTGGAACTAGTGATCC				
Section 23							
	(947)	947	960	970		989	
BCV N	(924)	ACAGTTCCCCATTCTTGCAGAAC - TCGCACCACAGCTGGTGC					
MHV N	(927)	ACAGTTCCCCATTCTTGCAGAGT - TGGCTCCAAGAGTTGGTGC					
Avian infectious bronchitis N	(798)	GC - GTGTTACAGCAATGCTCAAGCTTACACCAAGCCACATGC					
Consensus	(947)	ACAGTTCCCCATTCTTGCAGAAC	T	GCACCAACAGCTGGTGC			
Section 24							
	(990)	990	1000	1010	1020	1032	
BCV N	(966)	GTTTTCTTTTGGATCAAGATTAGAGTTGGCCAAAGTGCAGAAT					
MHV N	(969)	CTTCTCTTTTGGATCTAAATTAGAATTGGTCAAAA - - - AGAAT					
Avian infectious bronchitis N	(840)	TTGTCTTTTGGAGTAGAGT - GAC - - - GCCCAAG - - - - -					
Consensus	(990)	TTTTTCTTTTGGATCTAGATTAGA	TTGGCCAAAG	AGAAT			
Section 25							
	(1033)	1033	1040	1050	1060	1075	
BCV N	(1009)	TTGTCTGGGAATCTTGACGAGCCCCAGGAAGGATGTTTATGAAT					
MHV N	(1009)	T - - - CTGGTGGTGGTGCATCAACCCACCAAGATGTGTATGAGC					
Avian infectious bronchitis N	(871)	- - - - CT - - - TCAACAGATGGGCTTC - - - ACCTTAGATTTCGAAT					
Consensus	(1033)	T	CTGGT	ATCCTGATGAGCCCC	AA	GATGT	TATGAAT
Section 26							
	(1076)	1076	1090	1100		1118	
BCV N	(1052)	TGCGGTATAATCGTGCAATTAGATTTCACAGTACACTTTTCAGG					
MHV N	(1049)	TGCAATATTTCAGGTGCAGTTAGATTTCATAGTACTCTACCTGG					
Avian infectious bronchitis N	(905)	TT - ACTACTGGGTGGC - - - TAGAGATGACCCGCAGTTTGATAA					
Consensus	(1076)	TGCACTATT	TGGTGCA	TTAGATTTCACAGTAC	CTT	CTGG	
Section 27							
	(1119)	1119	1130	1140	1150	1161	
BCV N	(1095)	TTTTGAGACCATATA - - - - ATGAAGGTGTTGAATGAGAATTTTGAA					
MHV N	(1092)	TTTTGAGACTATC - - - - ATGAAGGTGTTGAATGAGAATTTTGAA					
Avian infectious bronchitis N	(945)	TTATGTAAAAATTTGTGATGAGTGTCTTTGATGCTGTAG - - GAA					
Consensus	(1119)	TTTTGAGAC	AT	ATGAA	GTGTTGAATGAGAATTTTGAA		
Section 28							
	(1162)	1162	1170	1180	1190	1204	
BCV N	(1134)	TGCATATCAACAACAAGATGCTAT - GATGAATATGA - GTCCAA					
MHV N	(1131)	TGCCTACCAGAAGGATGGTGGTGCACATGTGG - TGA - GCCCAA					
Avian infectious bronchitis N	(986)	CACGTCCAAAGGACGAAGTTGTAA - CACCAAGTCAACGCCCAA					
Consensus	(1162)	TGC	TACCAA	AACAAGGTGGTA	GATGAA	TGA	GCCCAA

**FIGURE 3A (contd.)**

						Section 29
	(1205)	1205	1210	1220	1230	1247
BCV N (1175)		AACCACAGCGTCA	---	GCGTGGTCAG	---	AAGAATGGACAAG
MHV N (1172)		AGCCCCAAAGAAAAGGGCGTAGACAGGCTCAGGAAAAGA	-	AAG		
Avian infectious bronchitis N (1028)		ATTCAAGAGCTGC	---	TACAAGAACAAG	-	TTCTCCAGCGCCAAG
Consensus (1205)		A CCACAACGT A		GCGTGGACAGG T A	GAA	GACAAG
						Section 30
	(1248)	1248	1260	1270	1280	1290
BCV N (1211)		GAGAAAATCATAATATAAGTGTTCAGCGCGTAAAAGCCGTGT				
MHV N (1214)		ATGAAGTAGATAATGTAAGCGTTGCCAAAGCCCCAAAAGCTCTGT				
Avian infectious bronchitis N (1068)		ACAACAGCGTCAAAAGAAGGAGAAGANGTCAAAGAAAGCAGGAT				
Consensus (1248)		A GAAA GATAATATAAG GTTGCAA GCC AAAAGC GTGT				
						Section 31
	(1291)	1291	1300	1310	1320	1333
BCV N (1254)		GCAGCAAAATAAGAGTAGAGAGTTGACTGCAGA	---	GGACATC		
MHV N (1257)		GCAGCGAAATGTAAGTAGAGAATTAAACCCAGA	---	GGATAGA		
Avian infectious bronchitis N (1111)		GATGAAGTAGATAAG	---	GCAATGACCTCAGATGAGGAGAGG		
Consensus (1291)		GCAGCAAAATATAAGTAGAGAATTGACC CAGA		GGA AG		
						Section 32
	(1334)	1334	1340	1350	1360	1376
BCV N (1294)		AGCCTTCT	---	TAAGAAGATGGATGA	-----	CCCCTATA
MHV N (1297)		AGTGTGTGGCTCAGATCCTTGATGATGGCGTAGTGGCAGATG				
Avian infectious bronchitis N (1150)		AACAATGCACAGCTGGAATTTGATGATGAACCCAAGGTGATTA				
Consensus (1334)		AGCCTT T TCAGAA TTGATGATG				GCC ATA
						Section 33
	(1377)	1377	1390	1400		1414
BCV N (1325)		CT	---	GAAGACACCTCAGAAATATAA	-----	
MHV N (1340)		GGTTAGAAGATGACTCTAATGTGTAA	-----			
Avian infectious bronchitis N (1193)		ACTGGGGGGATTTCAGCACTTGGAGAGAATGAGTTGTAA				
Consensus (1377)		T GAAGAT CCTCA ATGTATAA				
BCV N		SEQ ID NO: 9883				
MHV N		SEQ ID NO: 9894				
Avian infectious bronchitis N		SEQ ID NO: 9903				

**FIGURE 3B**

		Section 1				
		(1)	1	10	20	30 41
HOBMPRO	(1)	GATGTGGATGACGTTTAGGTAATCCAAACATTATGAGTAGT				
BCV M	(1)	-----				ATGAGTAGT
MHV M	(1)	-----				ATGACTAGT
Avian infectious brochitis virus M	(1)	-----				
Consensus	(1)					ATGAGTAGT
		Section 2				
		(42)	42	50	60	70 82
HOBMPRO	(42)	AAACTA	---	CTCCAGGACCAGTTTATATCTGGACTGCTGA		
BCV M	(10)	GTAAC	TA	---CACCAGCACCAGTTTACACCTGGACTGCTGA		
MHV M	(10)	ACCACTCAGGCTCCACAGCCTGTTTATCAGTGGACGGCTGA				
Avian infectious brochitis virus M	(1)	--ATGTC	---	CAACGCGGCAATTGCACTCTTGACTG-TGA		
Consensus	(42)	A AACTC		CTCCAGCGCCAGTTTATCTCTGGACTGCTGA		
		Section 3				
		(83)	83	90	100	110 123
HOBMPRO	(80)	TGAAGCTATTAAATTCCCTAAAGGAATGGAATTTTCTTTGG				
BCV M	(48)	TGAAGCTATTAAATTCCCTAAAGGAATGGAACTTTCTTTGG				
MHV M	(51)	TGAGGCAATTCGATTCCTTAAGGAATGGAATTTCTCTCTCG				
Avian infectious brochitis virus M	(36)	ACAGTCAGTTGAGCTTTTAAAGAATATAATTTATTTATAA				
Consensus	(83)	TGAGGCTATTAAATTCCCTTAAGGAATGGAATTTTCTTTGG				
		Section 4				
		(124)	124	130	140	150 164
HOBMPRO	(121)	GTATTATACTACTTTTTATTACAATCATATTGCAATTGGGA				
BCV M	(89)	GTATTATACTACTTTTTATTACAATCATATTGCAATTGGGA				
MHV M	(92)	GCATTATACTACTTTTTGTTACTATCATACTACAGITCGGT				
Avian infectious brochitis virus M	(77)	CCGCATTCCCTATTGTTTCTTACTATACTACTTCAGTATGGA				
Consensus	(124)	GTATTATACTACTTTTTATTACTATCATATTGCAGTTTGGGA				
		Section 5				
		(165)	165	170	180	190 205
HOBMPRO	(162)	TATACAAGTCGGAGTATGTTTGTGTTATGTTATTAAGATGAT				
BCV M	(130)	TATACAAGTCGGAGTATGTTTGTGTTATGTTATTAAGATGAT				
MHV M	(133)	TACACGAGCGGTAGCATGTTTGTGTTATGTTGTAAGAAATGAT				
Avian infectious brochitis virus M	(118)	TATGCAACAAGGAGTCGGTTTAAATTACATAATGAAAATGAT				
Consensus	(165)	TATACAAGTCGGAGTATGTTTGTGTTATGTTATTAAGATGAT				
		Section 6				
		(206)	206	220	230	246
HOBMPRO	(203)	TATTTTGTGGCTTATGTGGCCCTTACTATAATCTTAAC				
BCV M	(171)	CATTTTGTGGCTTATGTGGCCCTTACTATCATCTTAAC				
MHV M	(174)	ACTTTTGTGGCTTATGTGGCCACTAACTATGTTTGTGTA				
Avian infectious brochitis virus M	(159)	AGTGTTATGGTGCTTTTGGCCCTTAACATTGCAGTAGGTG				
Consensus	(206)	AATTTTGTGGCTTATGTGGCCCTTACTATTGTCTTAAGTA				

**FIGURE 3B (contd.)**

Section 7				
	(247) 247	260	270	287
HOBMPRO (244)	TTTTCAATTGCGTATACGCATTGAATAATGTGTATCTTGGC			
BCV M (212)	TTTTCAATTGCGTGTATGCGTTGAATAATGTGTATCTTGGC			
MHV M (215)	TTTTTAACCTGCGTCTATGCGCTAAATAATGTGTATCTTGGG			
Avian infectious brochitis virus M (200)	TAATTTTCATGTATATATCCACCAAATACAGGAGGTCTTGTG			
Consensus (247)	TTTTTAATTGCGTATATGCGTTGAATAATGTGTATCTTGGC			
Section 8				
	(288) 288	300	310	328
HOBMPRO (285)	CTTTCTATAGTTTTTTACCATAGTGGCCATTATTATGTGGAT			
BCV M (253)	TTTTCTATAGTTTTTCACTATAGTGGCCATTATCATGTGGAT			
MHV M (256)	TTTTCTATAGTGTTTACTATAGTGTCCATTATAATGTGGAT			
Avian infectious brochitis virus M (241)	GCAGCGAAAATACTTACAGTGGTTGCGTGTCTGTCTTTTGA			
Consensus (288)	TTTTCTATAGTTTTTACTATAGTGGCCATTAT ATGTGGAT			
Section 9				
	(329) 329	340	350	369
HOBMPRO (326)	TGTGTATTTTGTGAATAGTATCAGGTTGTTTATTAGAAGCTG			
BCV M (294)	TGTGTATTTTGTGAATAGTATCAGGTTGTTTATTAGAAGCTG			
MHV M (297)	TATGTATTTTGTGAATAGCATCAGGTTGTTTATCAGGACTG			
Avian infectious brochitis virus M (282)	AGGATATTGGATTTCAGAGTATCAGACTCTTTAAGCGGGGTG			
Consensus (329)	TGTGTATTTTGTGAATAGTATCAGGTTGTTTATTAGGACTG			
Section 10				
	(370) 370	380	390	400 410
HOBMPRO (367)	GAAGTTTTTTGGAGTTTGAACCCAGAAACAAACAACCTTGATG			
BCV M (335)	GAAGTTGGTGGAGTTTGAACCCAGAAACAAACAACCTTGATG			
MHV M (338)	GCAGCTGGTGGAGCTTCAACCCCGAAACAAACAACCTTAATG			
Avian infectious brochitis virus M (323)	GGCAATGGTGGGCATTTAACCCTGAGTCTAA - - - - TGCCG			
Consensus (370)	GAAGTTGGTGGAGTTTCAACCCAGAAACAAACAACCTTGATG			
Section 11				
	(411) 411	420	430	440 451
HOBMPRO (408)	TGTATAGATATGAAAGGAACAAATGTATGTTAGGCCGATAAT			
BCV M (376)	TGTATAGATATGAAGGGAAGGATGTATGTTAGGCCGATAAT			
MHV M (379)	TGTATAGATATGAAAGGTAAGTGTATGTTAGGCCGATAAT			
Avian infectious brochitis virus M (359)	T - - - - AGGT - TCAATACTCCTATCTA - - - - ATGGTCAACAAT			
Consensus (411)	TGTATAGATATGAAAGGTAAGTGTATGTTAGGCCGATAAT			
Section 12				
	(452) 452	460	470	480 492
HOBMPRO (449)	TGAGGACTATCATACTCTGACGGTCACAATAATACGCGGCC			
BCV M (417)	TGAGGACTACCATAACCTTACGGTCACAATAATACGTGGTC			
MHV M (420)	AGAGGATTACCATACACTAACAGCCACTATCATTCGTTGGTC			
Avian infectious brochitis virus M (392)	GTAATTTTGGTATAGA - - GAGTGTGCCAAT - - - - - GGTG			
Consensus (452)	TGAGGATTACCATACACTGACGGTCACAATAATACGTGGTC			

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**FIGURE 3B (contd.)**

Section 13					
(493)	493	500	510	520	533
HOBMPRO (490)	ATCTTTACATTCAAGGTATAAACTAGGTACTGGCTATTCT				
BCV M (458)	ATCTTTACATGCAAGGTATAAACTAGGTACTGGCTATTCT				
MHV M (461)	ACCTCTATATGCAAGGTGTTAAGCTAGGCACTGGCTTCTCT				
Avian infectious bronchitis virus M (424)	CTTTCT - - - - CCAATTATAAAGAATGGAGTTCTTTATTGT				
Consensus (493)	ATCTTTACATGCAAGGTATAAAGCTAGGTACTGGCTATTCT				
Section 14					
(534)	534	540	550	560	574
HOBMPRO (531)	TGGGCAGATTTCGCCAGCTTATATGAGTGTTCGTAAGGTAC				
BCV M (499)	TTGTCAGATTTCGCCAGCTTATGTGACTGTTCGTAAGGTCTC				
MHV M (502)	TTGTCTGATTTCGCTGCTTATGTTACAGTTGCTAAGGTGTCTC				
Avian infectious bronchitis virus M (460)	GAGGGTCAGTGGCTTGC - - - - TAAATGTGAACCAGACCAC				
Consensus (534)	TTGTCTGATTTCGCTGCTTATGTGACTGTTGCTAAGGTCTC				
Section 15					
(575)	575	580	590	600	615
HOBMPRO (572)	ACACCTGTGCACATATAAGCGTGGTTTTCTTGAAGGATAA				
BCV M (540)	ACACCTGTGCACATATAAGCGTGGTTTTCTTGAAGGATAG				
MHV M (543)	TCACCTTTGCACTTATAAGCGCGCATTCCTAGACAAGGTAG				
Avian infectious bronchitis virus M (496)	TTGCCTAAAGACATATTTG - - - - TTGCCCCACGATAG				
Consensus (575)	TCACCTGTGCACATATAAGCGTGGTTTTCTTGAAGGATAG				
Section 16					
(616)	616	630	640	656	
HOBMPRO (613)	GCGATACTAGTGGTTTTGCTGTTTATGTTAAGTCCAAAGTC				
BCV M (581)	GCGATACTAGTGGTTTTGCTGTTTATGTTAAGTCCAAAGTC				
MHV M (584)	ACGGTGGTTAGCGGTTTTGCTGTTTATGTTAAGTCCAAAGTC				
Avian infectious bronchitis virus M (531)	ACG-TAATA - - - - TCTACCGTATG-GTGCAG - - - AAATAC				
Consensus (616)	GCGATACTAGTGGTTTTGCTGTTTATGTTAAGTCCAAAGTC				
Section 17					
(657)	657	670	680	697	
HOBMPRO (654)	GGTAATTACCGACTGCCATCAACCCAAAAGGGTTCGGCAT				
BCV M (622)	GGTAATTACCGACTGCCATCAACCCAAAAGGGTTCGGCAT				
MHV M (625)	GGAAATTACCGACTGCCCTCAAATAAACCGAQT - - - GGCAT				
Avian infectious bronchitis virus M (562)	ACTGGTGACC-AAAGCGGAAATAAGAAAAGGTTTGCTACA -				
Consensus (657)	GGTAATTACCGACTGCCATCAACCCAAAAGGGTTCGGCAT				
Section 18					
(698)	698	710	720	738	
HOBMPRO (695)	GGACACCGCATTTGTTGAGAAATAATATCTAAATTTTAAGGA				
BCV M (663)	GGACACCGCATTTGTTGAGAAATAATATCTAA - - - - -				
MHV M (663)	GGACACCGCATTTGTTGAG - - - - - ATCTAA - - - - -				
Avian infectious bronchitis virus M (601)	- - - - -				
Consensus (698)	GGACACCGCATTTGTTGAGAAATAATATCTAA				
Section 19					
(739)					
HOBMPRO (736) TG	SEQ ID NO: 9912				
BCV M (694) - -	SEQ ID NO: 9884				
MHV M (688) - -	SEQ ID NO: 9895				
Avian infectious bronchitis virus M (601) - -	SEQ ID NO: 9904				
Consensus (739)					

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**FIGURE 3C**

Section 1							
	(1)	1	10	20	30	40	53
HOBHEGA	(1)	CTAAACTCAGTGAAAATGTTTTTGCTTCCTAGATTTATTCTAGTTAGCTGCAT					
BCV HE	(1)	CTAAACTCAGTGAAAATGTTTTTGCTTCCTAGATTTGTTCTAGTTAGCTGCAT					
MHV HE	(1)	-----					
Consensus	(1)	CTAAACTCAGTGAAAATGTTTTTGCTTC TAGATTT TTCTAGTTAGCTGCAT					
Section 2							
	(54)	54	60	70	80	90	106
HOBHEGA	(54)	AATTGGTAGCTTAGGTTTTTACAACTCTACCAATGTTGTTTCGGATGTAA					
BCV HE	(54)	AATTGGTAGCTTAGGTTTTTGACAATCCTCGTACCAATGTTGTTTCGCATTTAA					
MHV HE	(1)	-----					
Consensus	(54)	AATTGGTAGC TAGGTTTT ACAA CCTCCTACCAATGTTGTTTCGCAT TAA					
Section 3							
	(107)	107	120	130	140	159	
HOBHEGA	(107)	ATGGAGATTGGTTTTTATTTGGTGACAGTCGTTTCAGATTGTAATCATATTGTT					
BCV HE	(107)	ATGGAGATTGGTTTTTATTTGGTGACAGTCGTTTCAGATTGTAATCATATTGTT					
MHV HE	(1)	-----					
Consensus	(107)	ATGGAGATTGGTTTTTATTTGGTGACAGTCGTTTCAGATTGTAATCAT TTGTT					
Section 4							
	(160)	160	170	180	190	200	212
HOBHEGA	(160)	AATATCAACCCGCATAATTATCTTATATGGAGCTTAATCCTGTTCTGTGTGA					
BCV HE	(160)	ACTACCAACGGCCGTAATTATCTTATATGGAGCTTAATCCTGCCTTGTGTGG					
MHV HE	(1)	-----					
Consensus	(160)	A TA CAACCCCC TAATTATTCTTATATGGAGCTTAATCCTG TGTGTG					
Section 5							
	(213)	213	220	230	240	250	265
HOBHEGA	(213)	TTCTGGTAAAATATCATCTAAAGCTGGCAACTCCATTTTATAGGAGTTTTCAGT					
BCV HE	(213)	TTCTGGTAAAATATCATCTAAAGCTGGCAACTCCATTTTATAGGAGTTTTCAGT					
MHV HE	(1)	-----					
Consensus	(213)	TTCTGGTAAAATATCATCTAAAGCTGGCAACTCCATTTTATAGGAGTTTTCAGT					
Section 6							
	(266)	266	280	290	300	318	
HOBHEGA	(266)	TTACCGATTTTATAATTACACAGGCGAAGGTCAACAAATTATTTTATGAG					
BCV HE	(266)	TTACCGATTTTATAATTACACAGGCGAAGGTCAACAAATTATTTCTATGAG					
MHV HE	(1)	-----					
Consensus	(266)	TTACCGATTTTATAATTACACAGGCGAAGGTCAACAAATTATTTT TATGAG					
Section 7							
	(319)	319	330	340	350	360	371
HOBHEGA	(319)	GGTGTTAATTTTACGCCTTATCATGCCTTTAAATGCAACCGTTCTGGTAGTAA					
BCV HE	(319)	GGTGTTAATTTTACGCCTTATCATGCCTTTAAATGCAACCGTTCTGGTAGTAA					
MHV HE	(1)	-----					
Consensus	(319)	GGTGTTAATTTTACGCCTTATCATGCCTTTAAATGCA C TTCTGGTAGTAA					

**FIGURE 3C (contd.)**

							Section 8
	(372)	372	380	390	400	410	424
HOBHEGA	(372)	TGATATTTGGATGCAGAAATAAAGGCTTGT	TTTATACTCAGGTTTATAAGAATA				
BCV HE	(372)	TGATATTTGGATGCAGAAATAAAGGCTTGT	TTTACACTCAGGTTTATAAGAATA				
MHV HE	(1)	-----ATGGGCAATAAAGCTCGATTTTAT	GCCCGACTGTATGAGAAGA				
Consensus	(372)	TGATATTTGGATGCAGAAATAAAGGCTTGT	TTTATACTCAGGTTTATAAGAATA				
							Section 9
	(425)	425	430	440	450	460	477
HOBHEGA	(425)	TGGCTGTGTATCGCAGCCTTACTTTTGTTAATGT	ACCATATGTTTATAATGGC				
BCV HE	(425)	TGGCTGTGTATCGCAGCCTTACTTTTGTTAATGT	ACCATATGTTTATAATGGC				
MHV HE	(44)	TGGCCCAATATAGGAGCCTATCGTTTGTTAATGT	GTCTTATGCCCTATGGAGGT				
Consensus	(425)	TGGCTGTGTATCGCAGCCTTACTTTTGTTAATGT	ACCATATGTTTATAATGGC				
							Section 10
	(478)	478	490	500	510	520	530
HOBHEGA	(478)	TCTGCACAATCTACAGCTCTTTTGTAATCTGGTAG	TTTACTTCTTAATAACCC				
BCV HE	(478)	TCTGCACAATCTACAGCTCTTTTGTAATCTGGTAG	TTTACTTCTTAATAACCC				
MHV HE	(97)	AATGCAAAGCCCGCCTCATTTCGCAAGACAATACT	TTAACACTCAATAACCC				
Consensus	(478)	TCTGCACAATCTACAGCTCTTTTGTAATCTGGTAG	TTTACTTCTTAATAACCC				
							Section 11
	(531)	531	540	550	560	570	583
HOBHEGA	(531)	TGCATATATAGCTCCTCAAGCTAACTCTGGGATTAT	TATTATAAGGTTGAAG				
BCV HE	(531)	TGCATATATAGCTCGTGAAGCTAATTTTGGGATTAT	TATTATAAGGTTGAAG				
MHV HE	(150)	CACCTTCATATCGAAGGAGTCTAATTATGTTGATTAT	TACTATGAGAGTGAGG				
Consensus	(531)	TGCATATATAGCTC	TGAAGCTAATT	TGGGATTATTATTATAAGGTTGAAG			
							Section 12
	(584)	584	590	600	610	620	636
HOBHEGA	(584)	CTGATTTTATTTTGTTCAGGTTGTGACGAGTATATCGT	ACCCTTTGTATTTTT				
BCV HE	(584)	CTGATTTTATTTTGTTCAGGTTGTGACGAGTATATCGT	ACCCTTTGTATTTTT				
MHV HE	(203)	CTAATTTACACTAGAAAGGTTGTGATGAATTTATAGTAC	CGCTCTGTGGTTTT				
Consensus	(584)	CTGATTTTATTTTGTTCAGGTTGTGACGAGTATATCGT	ACCCTTTGTATTTTT				
							Section 13
	(637)	637	650	660	670	689	
HOBHEGA	(637)	AACGGCAAGTTTTTG-----TCCAATACA-----	AAGTATTATGATGA				
BCV HE	(637)	AACGGCAAGTTTTTG-----TCCAATACA-----	AAGTATTATGATGA				
MHV HE	(256)	AATGGCCATECCAAGGGCAGCTCTTCGGATGCTGCCAATAA	TATTACTCA				
Consensus	(637)	AACGGCAAGTTTTTG	TCCAATACA	AAGTATTATGATGA			
							Section 14
	(690)	690	700	710	720	730	742
HOBHEGA	(675)	TAGTCAATATTATTTTAATAAAGACACTGGTGTTATTTAT	GGTCTCAATTCTA				
BCV HE	(675)	TAGTCAATATTATTTTAATAAAGACACTGGTGTTATTTAT	GGTCTCAATTCTA				
MHV HE	(309)	CTCTCAGAGTTACTATAATATGGATATGGTGTCCTTATAT	GGGTTCAATTCTA				
Consensus	(690)	TAGTCAATATTATTTTAATAAAGACACTGGTGTTATTTAT	GGTCTCAATTCTA				



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**FIGURE 3C (contd.)**

								Section 15
	(743)	743	750	760	770	780	795	
HOBHEGA	(728)	C	-----	AGAAACCATTA	CCA-----	CTGGTTTTGATCTTAA	TTGTTAT	
BCV HE	(728)	C	-----	TGAAACCATTA	CCA-----	CTGGTTTTGACTTTAA	TTGTCA	
MHV HE	(362)	C	CTTGGATGTTGGCAACACTGCTAAGGATCCGGGTCTTGATCTCACTTGCAGG					
Consensus	(743)	C		TGAAACCATTA	CCA	CTGGTTTTGATCTTAA	TGT AT	
								Section 16
	(796)	796	810	820	830	848		
HOBHEGA	(766)	TATTTAGTTTTAC	CCTCTGGTAATTATTTAGCCATTTCAAATGAGCTATTGTT					
BCV HE	(766)	TATTTAGTTTCTA	CCTCTGGTAATTATTTAGCCATTTCAAATGAGCTATTGTT					
MHV HE	(415)	TATCTTGCA	TGACTCCTGGTAATTATAAGGCTGTGTCTTAGAATATTGTT					
Consensus	(796)	TATTTAGTTTTAC	CCTCTGGTAATTATTTAGCCATTTCAAATGAGCTATTGTT					
								Section 17
	(849)	849	860	870	880	890	901	
HOBHEGA	(819)	A	ACTGTTCTTACGAAAGCAATCTGTCTTAATAAGCGTAAGGATTTTACGCCTG					
BCV HE	(819)	A	ACTGTTCTTACTAAAGCAATCTGTCTTAATAAGCGTAAGGATTTTACGCCTG					
MHV HE	(468)	A	AGCTTACCCTCAAAGGCTATTTGCCATCCATAAGACAAAGCGCTTTATGCCG					
Consensus	(849)	A	ACTGTTCTTAC	AAAGCAATCTGTCTTAATAAGCGTAAGGATTTTACGCCTG				
								Section 18
	(902)	902	910	920	930	940	954	
HOBHEGA	(872)	TACAGGTTGTTGATT	CGCGGTGGAACAATGCCAGGCAGTCTGATAACATGACG					
BCV HE	(872)	TACAGGTTGTTGATT	CGCGGTGGAACAATGCCAGGCAGTCTGATAACATGACG					
MHV HE	(521)	TGCAGGTAGTTGACTCAAGGTGAGTAGCATGCCAGTCAGACAATATGACC						
Consensus	(902)	TACAGGTTGTTGATT	CGCGGTGGAACAATGCCAGGCAGTCTGATAACATGACG					
								Section 19
	(955)	955	960	970	980	990	1007	
HOBHEGA	(925)	G	CGGTTGCTTGTC	AACCTCCGTACTGTTATTTTCGTAATTCTACTACCACTA				
BCV HE	(925)	G	CAGTTGCTTGTC	AACCCCCGTACTGTTATTTTCGTAATTCTACTACCACTA				
MHV HE	(574)	G	CTGCAGCCGTCAGCTGCCATATTGTTTCTTTGCAACACATCTGCGAATTA					
Consensus	(955)	G	CTTGCTTGTC	AACC	CGTACTGTTATTTTCGTAATTCTACTACCAATTA			
								Section 20
	(1008)	1008	1020	1030	1040	1050	1060	
HOBHEGA	(978)	TGTTGGTGTTT	---ATGATATTAATCATGGAGATGCTGGTTTTACTAGCATAC					
BCV HE	(978)	TGTTGGTGTTT	---ATGATATTAATCATGGGATGCTGGTTTTACTAGCATAC					
MHV HE	(627)	TAGTGCTGGCACACATGATGCGCACCATGGTGATTTTCATTTCAAGGCAGTTAT						
Consensus	(1008)	TGTTGGTGTTT	ATGATAT	AATCATGG	GATGCTGGTTTTACTAGCATAC			
								Section 21
	(1061)	1061	1070	1080	1090	1100	1113	
HOBHEGA	(1028)	T	TAGTGGTTTGTTATATAATTCACCTTGTTTTTCGCAGCAAGGCGTTTTTAGG					
BCV HE	(1028)	T	CAGTGGTTTGTTATATGACTCAACCTTGTTTTTCGCAGCAAGGCGTTTTTAGG					
MHV HE	(680)	T	GCTCGTTTGTTATATAAGTTCCTGTATTGCCAGCAGGGTGCAATTTCTT					
Consensus	(1061)	T	AGTGGTTTGTTATATAATTCACCTTGTTTTTCGCAGCAAGGCGTTTTTAGG					

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**FIGURE 3C (contd.)**

							Section 22
(1114)	1114	1120	1130	1140	1150	1166	
HOBHEGA (1081)	TATGATAATGTTAGCAGTGTCTGGCCTCTCTACCCCTATGGCAGATGTCCCAG						
BCV HE (1081)	TATGATAATGTTAGCAGTGTCTGGCCTCTCTACCCCTATGGCAGATGCCCTAC						
MHV HE (733)	TATAATAATGTTAGTTCCTCTTGGCCAGCCCTATGGGTACGGTCATTGTCCAAC						
Consensus (1114)	TATGATAATGTTAGCAGTGTCTGGCCTCTCTACCC TATGGCAGATGTCC AC						
							Section 23
(1167)	1167	1180	1190	1200		1219	
HOBHEGA (1134)	TGCTGCTGATATTAATAACCCTGATTTACCCATTTGTGTGTATGATCCGCTAC						
BCV HE (1134)	TGCTGCTGATATTAATAACCCTGATGTACCTATTTGTGTGTATGATCCGCTAC						
MHV HE (786)	GGCAGCTAACATTGGTTA - - - TATGGCACCCTGTTTGTATCTATGACCCTCTCC						
Consensus (1167)	TGCTGCTGATATTAATAACCCTGATGTACCTATTTGTGTGTATGATCCGCTAC						
							Section 24
(1220)	1220	1230	1240	1250	1260	1272	
HOBHEGA (1187)	CAGTTATTTTGCTTGGCATTCTTTTGGGCGTTGCGGTCATAATTATTGTAGTT						
BCV HE (1187)	CAATTATTTTGCTTGGCATTCTTTTGGGCGTTGCGGTCATAATTATTGTAGTT						
MHV HE (836)	CGGTCATACTGCTAGGTGTGTTATTGGGTATAGCTGTGTTGATTATTGTGTTT						
Consensus (1220)	CAGTTATTTTGCTTGGCATTCTTTTGGGTGTTGCGGTCATAATTATTGTAGTT						
							Section 25
(1273)	1273	1280	1290	1300	1310	1325	
HOBHEGA (1240)	TTGTTGTTATATTTTATGGTGGATAAATGGTACTAGGCTGCATGATGCTTAGAC						
BCV HE (1240)	TTGTTGTTATATTTTATGGTGGATAAATGGTACTAGGCTGCATGATGCTTAGAC						
MHV HE (889)	TTGATGTTTATATTTTATGACGGATAGCCGGTGTAGATTGCATGAGGCATAA - -						
Consensus (1273)	TTGTTGTTATATTTTATGGTGGATAAATGGTACTAGGCTGCATGATGCTTAGAC						
							Section 26
(1326)	1326	1337					
HOBHEGA (1293)	CATAATCTAAAC		SEQ ID NO: 9913				
BCV HE (1293)	CATAATCTAAAC		SEQ ID NO: 9885				
MHV HE (940)	-----		SEQ ID NO: 9896				
Consensus (1326)	CATAATCTAAAC						

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**FIGURE 4****FIGURE 4A**

		Section 1			
		(1) 1	10	20	39
avian infectious bronchitis pol 1ab	(1)	-----			
bovine coronavirus pol 1ab	(1)	MSKLNKYGLELHWAFEPWPFEDAEKIDNRSSEVDIV			
Human corona 229E pol 1ab	(1)	-----MACNRVTLAVASDSEISANG			
Murine hepatitis pol 1ab	(1)	MAKMGKYGGLGFKWAFEPFWMPLNASEKDGNERSEEDGF			
Consensus	(1)	MAKI KYGL WAFEPFWM NA EKL NPDSE D			
		Section 2			
		(40) 40	50	60	78
avian infectious bronchitis pol 1ab	(1)	-----			
bovine coronavirus pol 1ab	(40)	CSTTAOKLETGGICPENHYMDCRRLLKQEGCVQSLLTR			
Human corona 229E pol 1ab	(21)	CSTIAQAARRYSEAAASNGFACRFVSLDLCDCIVGIADD			
Murine hepatitis pol 1ab	(40)	CSAAQEPKVKGKTLVNHVRVNGSRIPALEGCVQSATFR			
Consensus	(40)	CST AQ LK G NHVRV C RLL LECCVQSATIR			
		Section 3			
		(79) 79	90	100	117
avian infectious bronchitis pol 1ab	(1)	-----			
bovine coronavirus pol 1ab	(79)	ELVMNTRPYDLEVLLODALOSREAVLVTPPLGMSLEACY			
Human corona 229E pol 1ab	(60)	TYVMGLHGNOTLFCNIMKFSDEPFMIHG-----WLVEFS			
Murine hepatitis pol 1ab	(79)	DEFDDEDQKVEASTMMALQFGSAVLVKESKRISTQANT			
Consensus	(79)	DIVM FN LE IMAIQ R AVL V P LSI AFS			
		Section 4			
		(118) 118	130	140	156
avian infectious bronchitis pol 1ab	(1)	-----HASSLKQGVSPK-----PRDVILMSKDI			
bovine coronavirus pol 1ab	(118)	VRGCNPNMTMGLERRRSVNTGRCAYNKHVAYQLYMID			
Human corona 229E pol 1ab	(93)	NSNYLLEEDDVVFGRR-----GGNVITYTDQYLCGADG			
Murine hepatitis pol 1ab	(118)	NLGVLPRTAAMGLEKRVCLCNTREOSCDAHVAEHLETVO			
Consensus	(118)	N G LP SF MGLFRR LCNTG CAV HVAYLLF D			
		Section 5			
		(157) 157	170	180	195
avian infectious bronchitis pol 1ab	(24)	PEOLCDALFFETSHNPKDYADAFVROKEDRSLOTGKQF			
bovine coronavirus pol 1ab	(157)	PAGVCFGAGQEVGVLPPLAFMPVQSRKPTVPAWVMYLRKC			
Human corona 229E pol 1ab	(126)	KPVMSDDLWQFVDHEGENEELITNGHTYVCAMITKRKPL			
Murine hepatitis pol 1ab	(157)	PDGVCLGNGFPLGWEVPTALPEYAKOWLOQPMSTLLRKQ			
Consensus	(157)	PDGVCDGLGQFVGWFIPLAIPINARQFI PWLI LKK			
		Section 6			
		(196) 196	210	220	234
avian infectious bronchitis pol 1ab	(63)	KEET-----VC--GLFLLKGVDKITPGVPARV			
bovine coronavirus pol 1ab	(196)	GEKG-AYNKDHKRGGEFHVYNFKVEDAYDLVHDEPKGKE			
Human corona 229E pol 1ab	(165)	DYKR-----Q--NNLAIEEIEYMHGDALHTLR			
Murine hepatitis pol 1ab	(196)	GNKGSVTSGFERRAVTMPVYDFNVEDACEEVHLNPKGKY			
Consensus	(196)	GFKG KRA M VYNL VEDA DLVHDAPKGKE			

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**FIGURE 4A (contd.)**

						Section 7
	(235)	235	240	250	260	273
avian infectious bronchitis pol 1ab	(88)	LKATSKLADLEDIFGVSPHARNYRELLKTACQWSLTVEA				
bovine coronavirus pol 1ab	(234)	SKKAYALIRGYRGVKPLLYVDQYGC DYTGGLADGLEA YA				
Human corona 229E pol 1ab	(190)	NGSVLEMAKEVKTS SKVVLSDALDKLYKVFGSPVMTNGS				
Murine hepatitis pol 1ab	(235)	SKKAYALLKGYRGVKRIEFVDQYGC DYTGCLAKGLEDY G				
Consensus	(235)	SKKAYALAKGYRGVKPILLVDQYGC LYTGALA GLT YA				
						Section 8
	(274)	274	280	290	300	312
avian infectious bronchitis pol 1ab	(127)	LDVRAQTLDEIFDPTETLWLQVAAKIEVSSMAMRRITVGE				
bovine coronavirus pol 1ab	(273)	DKTLEQMKALEPTIMSCBEPFDVTVAWHVVRDPRYVMRLQ				
Human corona 229E pol 1ab	(229)	NILEAFTKPVFISALVQCTCGTKSWSVGDWTGFKSSCCN				
Murine hepatitis pol 1ab	(274)	DITLSEMKELEPVRWDSIDSEVLVAWHVDRDPRAMRLQ				
Consensus	(274)	DITLAETKDLFPWSD L DV VAWHVDRDPRKAMRLQ				
						Section 9
	(313)	313	320	330	340	351
avian infectious bronchitis pol 1ab	(166)	VTAKVMDAIGSNLSALFQIVKQQTARIFOKATAIFENVN				
bovine coronavirus pol 1ab	(312)	SASTIRSMAYVANPTEDECDGSSVVIKEEPVHVYADDSITL				
Human corona 229E pol 1ab	(268)	VTSNKLGVVPGNVKFGDAMITIQQAGAGIKYFCGMTLKF				
Murine hepatitis pol 1ab	(313)	TATVRCEDYVVGQPTEDVVDGQVVVREPANILLANAIVK				
Consensus	(313)	VIATVRCVLYVNQPTEDLVDGSSVAREPIKLLAA SIV				
						Section 10
	(352)	352	360	370	380	390
avian infectious bronchitis pol 1ab	(205)	ELPQRTAALKMAFAKCARSTTVVVVERTLVVKEFAGTCL				
bovine coronavirus pol 1ab	(351)	RQHNLVDIMSCFYMEADAVVNATYGVDLKDCGGEVMOEGY				
Human corona 229E pol 1ab	(307)	VAN-----IEGVSVWRVTALQSVDCFVASSTEVE				
Murine hepatitis pol 1ab	(352)	RLP---RLVETMLYTDSSVTEFCMKTKICEGGEITQFCY				
Consensus	(352)	RLPN I IL FIEAASVI VIYL KL DCGFISQFGY				
						Section 11
	(391)	391	400	410		429
avian infectious bronchitis pol 1ab	(244)	ASINGAVAKTFEELPNEGFMGSKIFTTLAFFKEAAVRYVE				
bovine coronavirus pol 1ab	(390)	IDCEQDLCDFKGVVPCNMIDGFACTTCGHVYETGDLTAQ				
Human corona 229E pol 1ab	(336)	EEHVNRMDTECFNVRNMTDECRLAMTGAEMTSNVRQV				
Murine hepatitis pol 1ab	(388)	VDCCGDTCDERGVVACNMMDGEPGPGCTKNYMPWELEAQ				
Consensus	(391)	IDC GDLCDFKGVVFNMMMDGE CTTLG YESAVRLAQ				
						Section 12
	(430)	430	440	450		468
avian infectious bronchitis pol 1ab	(283)	NIPNAPRGTKGFEVVGNAKGTQVVVRGMRNDLTLLDOKA				
bovine coronavirus pol 1ab	(429)	SSGVLPVNPVLHTKSAAGYGGFGCKDSFTLYGQTVVYFG				
Human corona 229E pol 1ab	(375)	ASGVLDISTGWEDVYDDIFAE-----SK-PWFVRKA				
Murine hepatitis pol 1ab	(427)	SSGVLPREGGVLEFQSTDTVN----RESERKLYGHAVVPG				
Consensus	(430)	SSGVIPIGTVLFTVSADAFG KDSFKLYG VV KA				

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**FIGURE 4A (contd.)**

Section 13						
	(469)	469	480	490	507	
avian infectious bronchitis pol 1ab	(322)	DIPVEFEGWSA	ILDGHL	CYVFRSGDRFYAAP	LSGNFALS	
bovine coronavirus pol 1ab	(468)	GCVYWS-	PARNIWIPI	LKSSVK	SYDGLVYTG	
Human corona 229E pol 1ab	(405)	EDIEGP-	CWSA	ASALKQLKVT	TGELVREVKSECNSAVA	
Murine hepatitis pol 1ab	(462)	SAVYWS-	PCPGMNL	EVHWSSVK	SYSGLTYYTG	
Consensus	(469)	D	VYWS	PWSAIWIPIL	SSVKS	
Section 14						
	(508)	508	520	530	546	
avian infectious bronchitis pol 1ab	(361)	DVHCCERVV	CLSDGVTPEIND	GLILAATYSS	SFSVSELVA	
bovine coronavirus pol 1ab	(506)	KETNLICKA	LYLDYVQHKCGNI	HOREEL	GVSDVWHKOLL	
Human corona 229E pol 1ab	(443)	VVGGT	LQILAS	MPKFLNAFDM	FVTA	
Murine hepatitis pol 1ab	(500)	QETDAICRS	LYMDYVQHKCGN	LEORATLGE	DDVYHFOIL	
Consensus	(508)	VT	ICRS	LYLDYVQHKCGNL	QRAILGVSDVWHEQLT	
Section 15						
	(547)	547	560	570	585	
avian infectious bronchitis pol 1ab	(400)	ALRKGEPFK	ELGHKFPYAKDAAMS	FTLAKAATIAD	VLRL	
bovine coronavirus pol 1ab	(545)	ENRGVYKPL	LENIDYENMRR	AKFSLETETV	CADGFMPL	
Human corona 229E pol 1ab	(482)	TAGKAFDKV	DYVLLDNALV	KLVMTTKIKGV	RERGLNKVK	
Murine hepatitis pol 1ab	(539)	VNRGDYSL	LENVDL	EVKRRABFAC	-EATCGDGIVBET	
Consensus	(547)	INRKAY	LENVDLFNARRA	VS	KLF	
Section 16						
	(586)	586	600	610	624	
avian infectious bronchitis pol 1ab	(439)	EQSARVIAED	VWSSFTEKSF	FEFWKLA	YGVKVRNLEEFVKT	
bovine coronavirus pol 1ab	(584)	LDLVP	RAYGLAVSGQAF	CDYADKIC	HAVVSKSKELLDV	
Human corona 229E pol 1ab	(521)	YATVVG	STEEVKSS	-----	RVERSTAVLTIANNYSKL	
Murine hepatitis pol 1ab	(577)	LDGLVPR	SYLIRKSGQAF	TSMMVN	SHEVTUMCMQMALI	
Consensus	(586)	LD	SLVVRAYYLIRKSGQAFS		VKISHAVVSIA	
Section 17						
	(625)	625	630	640	650	663
avian infectious bronchitis pol 1ab	(478)	YVCKAQM	STVILA	AAVLGEDI	WHLVS---	QVLYKLGVLFT
bovine coronavirus pol 1ab	(623)	SLDSL	SAATHY	LN	SKIVDLAQHF	SDFGTSFVSKIVHEEK
Human corona 229E pol 1ab	(554)	FDEGYT	VVIGDMAYFV	SDGYER	LMASPN	SVLTTAVYKPL
Murine hepatitis pol 1ab	(616)	FMHDM	VATKYVK	KVTGKLAVR	KALGVAVVR	KITEWED
Consensus	(625)	FLD	LSVAI	YLA	AVIGDLA	FLMA
Section 18						
	(664)	664	670	680	690	702
avian infectious bronchitis pol 1ab	(514)	KVVDF	CDKHKKGF	CVOLKRAK	LIVTET	FCVLKGVAQHCF
bovine coronavirus pol 1ab	(662)	TFTT	STALAF	AWVLEHV	ELHQA	YIVVESDYEYVKNLPRYA
Human corona 229E pol 1ab	(593)	FAFN	VNV	MGTR	PEKEPTT	VTCE
Murine hepatitis pol 1ab	(655)	LAVD	IAASAAG	MDCYOL	VNGL	FAVANC
Consensus	(664)	AVDI	ALAFKWL	CFQLL	G	FIV

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**FIGURE 4A (contd.)**

Section 19						
	(703)	703	710	720	730	741
avian infectious bronchitis pol 1ab	(553)	QLLLDAIHSLYKSFKKCALGRTHGULLFWKGGVHKIVQD				
bovine coronavirus pol 1ab	(701)	SAVAQAERSVAKVLDSELRVTTFIDGLSCPKIGRRRTCLS				
Human corona 229E pol 1ab	(632)	LDYSIDVIDONEIIVKPNISLCVPLYVRDYVDKWDDEFGRQ				
Murine hepatitis pol 1ab	(694)	KNFVQKEKAFERKVLIDSMSVSILSGLTVVKTAASNRVCLA				
Consensus	(703)	VSDAFKSLFKVVKDSISVSII	GLS	FK	G	RICLA
Section 20						
	(742)	742	750	760	770	780
avian infectious bronchitis pol 1ab	(592)	GD-----				
bovine coronavirus pol 1ab	(740)	GSKIYEVEERGLLHSSQLPLDVYDLTMPSEQVQKAKQKPIY				
Human corona 229E pol 1ab	(671)	YS-----				
Murine hepatitis pol 1ab	(733)	GSKVYEPVQKSLSAAYVMPVGCSEATCLVGEIEP-----				
Consensus	(742)	GSKIYEV	L A	LPL	D T	
Section 21						
	(781)	781	790	800	819	
avian infectious bronchitis pol 1ab	(594)	-----EIMFDAHDSVDMEDEGMVQEKSLDFEVMGD				
bovine coronavirus pol 1ab	(779)	LKSGSGSDFSLADSVVEVVTTSITPCGYSEPPKMAADKICI				
Human corona 229E pol 1ab	(673)	-----NESWFEDDYRAFTSVLEDTDAAVKAAESKA				
Murine hepatitis pol 1ab	(766)	-----AVFEDDVVDVVKAPLTYQGCKEPEESFEKICI				
Consensus	(781)		EDWVVDVVS	A LT	LGISDPPPSIADKICI	
Section 22						
	(820)	820	830	840	858	
avian infectious bronchitis pol 1ab	(623)	DMTEPENQPGHMMVQIEDDGKNYMFFRFKKDENIYYTPMS				
bovine coronavirus pol 1ab	(818)	VDNVYMAKAGDKYYPVVVDG-HVGLLDQAWRVPCAGRRV				
Human corona 229E pol 1ab	(703)	FVDTIMPPCPSELKVLIDGGKIWNGVINKVNSMRDWLKS				
Murine hepatitis pol 1ab	(798)	VDKLYMAKCGDQFPPVVVNDTGVLDQCWRFPFCAGKKV				
Consensus	(820)	VV	LYMAKCGDIVYPVVVGK	WVGVLQ	WRVPCAGKKV	
Section 23						
	(859)	859	870	880	897	
avian infectious bronchitis pol 1ab	(662)	QIFGAINVCKAGGKTVTFGETTVQEIIPPPDVVPIKVSIE				
bovine coronavirus pol 1ab	(856)	TEHQQTVNEEASTPKTKVVFELDKDENITIENTACVFE				
Human corona 229E pol 1ab	(742)	KENLTQQGLLGTCARFRKRWLGTFLEAYNAFLDTVVSTV				
Murine hepatitis pol 1ab	(837)	EINDKPKVRKTFST-RKIKLTFALDATEDSVLSKACSEF				
Consensus	(859)	LND P V	KIAST	RTIKITFILD	FNSVL TAVSIF	
Section 24						
	(898)	898	910	920	936	
avian infectious bronchitis pol 1ab	(701)	CCGEPWN-----TFKKAYKEPIEVDTDITVEQLLSV				
bovine coronavirus pol 1ab	(895)	EVD DTVDMEEFYAVVIDAIEEKLSPCKELEGVGAKVSAF				
Human corona 229E pol 1ab	(781)	RIGG-----LTFKLYAFDKPIVIRDIVCKV				
Murine hepatitis pol 1ab	(875)	EVDKDYTLDELLEDVLDVAVESTESPECKEHDVIGTKVCAL				
Consensus	(898)	EVGD V LDE	VVIDAIE	TLSPCKEHDVIGDKVCAV		

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**FIGURE 4A (contd.)**

						Section 25
						(937) 937 950 960 975
avian infectious bronchitis pol 1ab	(733)	IYEKMCDDIKKREAPPPPPFENVALVDKNGKLLDCHIKS				
bovine coronavirus pol 1ab	(934)	LOKLEUNSLLELDEAGEEVLASKLYCAFTAPEDDDFLKEE				
Human corona 229E pol 1ab	(807)	ENKTEAEWTELEFRRNDRIKSESTTESAYMPIADPTHEDI				
Murine hepatitis pol 1ab	(914)	LDRUAGDYVYTFDEGGDEVTAAPMYCSFSAPEDEDCMAA				
Consensus	(937)	LNKLEADWLFLFPEAGEEVIFSKLYCAFSAPDDDDCIDA				
						Section 26
						(976) 976 990 1000 1014
avian infectious bronchitis pol 1ab	(772)	CHLIYKDYFSDDDIIEEDAECDTDSGEALCEDTN----				
bovine coronavirus pol 1ab	(973)	SGVEEDDVGEETDLIVTSAGEPCVASEQEE-----				
Human corona 229E pol 1ab	(846)	EEVELLDAAEFVEPGCGGLAVIDENHVFYKADGVYYP---				
Murine hepatitis pol 1ab	(953)	DVVDADENQDDDAEDSAVLAADTQEE DGVAKGQVEADSE				
Consensus	(976)	D VE DD E DD DDSAILAADD DA E EEG				
						Section 27
						(1015) 1015 1020 1030 1040 1053
avian infectious bronchitis pol 1ab	(807)	-----SECEEDEDTKVLALLQDPASTKRYPLPLEDE				
bovine coronavirus pol 1ab	(1004)	-----SSEILEDTLDDGPCVETSDSQVEEDVEMSDFADEE				
Human corona 229E pol 1ab	(882)	-----SNGTNILPVAFTRAAAGKVSFSDDEVKDIEPMY				
Murine hepatitis pol 1ab	(992)	ICVAHTGSSELAEPDAVGSOPTFASAEETEVGEASDRE				
Consensus	(1015)	S SEDL EDD AA A IQ AEDVEV D ADLE				
						Section 28
						(1054) 1054 1060 1070 1080 1092
avian infectious bronchitis pol 1ab	(838)	YSVYNGCIIVHKDAEDVNLPSG-----				
bovine coronavirus pol 1ab	(1039)	SVIQDYENVCFEFYTTEP-----				
Human corona 229E pol 1ab	(916)	RVKLCPEFEDEKLYDVCEKATG-----				
Murine hepatitis pol 1ab	(1031)	GTAEAKATVGADAVDACPDQVEAFEIEKVEDSILDELQT				
Consensus	(1054)	VI FE VC DAVDVCP IG				
						Section 29
						(1093) 1093 1100 1110 1120 1131
avian infectious bronchitis pol 1ab	(860)	-----EE				
bovine coronavirus pol 1ab	(1057)	-----EFVKV				
Human corona 229E pol 1ab	(938)	-----KKIK				
Murine hepatitis pol 1ab	(1070)	ELNAPADKTYEDVLAFDAVCSEALSAFYAVPSDETHFKV				
Consensus	(1093)	KV				
						Section 30
						(1132) 1132 1140 1150 1160 1170
avian infectious bronchitis pol 1ab	(862)	TFMVN-----NCFEGAVKPLPQKVMVDV				
bovine coronavirus pol 1ab	(1062)	LDLYVRKATRNNCWLRSVLAVMOKLPCQFKDKNLQDLWV				
Human corona 229E pol 1ab	(942)	HEG-----DWDSECKTQSALSVVSCYVNLPTYYL				
Murine hepatitis pol 1ab	(1109)	CGFYSPAERTNCWLRSTLIIMQSTPLEFRDLFMOKLWL				
Consensus	(1132)	DLY P R NCWLR L VMQALPL FKDLNLQ LWV				

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**FIGURE 4A (contd.)**

Section 31					
	(1171)	1171	1180	1190	1209
avian infectious bronchitis pol 1ab	(884)	LGDWGEAVDAQEQLCQOEFLQHTFEEPVENSTGSSKTM			
bovine coronavirus pol 1ab	(1101)	LYKQOYSOLFVDTLVNKEFLANIVVPQGGYVADFAYWELT			
Human corona 229E pol 1ab	(972)	YDEEGGNOLSLPVMISEWELSVQQAQCEATLPDIAEDMV			
Murine hepatitis pol 1ab	(1148)	SYKAGYDQCFLVDKLVKSVFKSITLPPGGYVADFAYEPLS			
Consensus (1171)		LYK GYAQLFVD LVN IPLSIILPQGGYVADFAYFFLT			
Section 32					
	(1210)	1210	1220	1230	1248
avian infectious bronchitis pol 1ab	(923)	EOVVVEDQELPVVEQODVVVYTPPTDLEVAKETAEEVDE			
bovine coronavirus pol 1ab	(1140)	LCDWQCVAYNKCICDALKLKGLDAMFFYGDVVSHVCK			
Human corona 229E pol 1ab	(1011)	DOVEEVNSIEDIETVVKHNVSPFEMPFEELNGLKILKQ			
Murine hepatitis pol 1ab	(1187)	QCSEKAYANWRCLCECMEEKLOGLDAMFFYGDVVSHMCK			
Consensus (1210)		DQVF A WKCIECDLCLKL GLDAMFFYGDVVSHVCK			
Section 33					
	(1249)	1249	1260	1270	1287
avian infectious bronchitis pol 1ab	(962)	FILIFAMPKEEVVSQKDGAIKQEPQVVKPQRE-KK--			
bovine coronavirus pol 1ab	(1179)	CGESMVLTDVDVPETAHFALKKLECAEITKRSMYKAAC			
Human corona 229E pol 1ab	(1050)	LDNNCWVNSVMLOIQITGILGGDYAMQEFKMG-----			
Murine hepatitis pol 1ab	(1226)	CGNSMTLLS DITPYTLHFGVRDDKFCAPYTPRKVERAAC			
Consensus (1249)		CGNSM LISVDVPFTLHGALKDD FCQFVTPRKVFKAAC			
Section 34					
	(1288)	1288	1300	1310	1326
avian infectious bronchitis pol 1ab	(998)	-----			AK
bovine coronavirus pol 1ab	(1218)	VVDVNDSHSMAVVDGKQIDDDRVSITSDFDFIIGHGM			
Human corona 229E pol 1ab	(1082)	-----			
Murine hepatitis pol 1ab	(1265)	AVDVNDCHSMAVVEGKQIDGKVVTKFIGDKEDFEMVGYGM			
Consensus (1288)		VDVND HSMVVDGKQID VT DKFDFIIGHGM			
Section 35					
	(1327)	1327	1340	1350	1365
avian infectious bronchitis pol 1ab	(1000)	KEKVKBATCERPKFLEKTCVGDLTVVIAKALDEFKEFC			
bovine coronavirus pol 1ab	(1257)	SFSMTTEETAQLYGSGITPNVCFVKGDIKVSRRVKAEV			
Human corona 229E pol 1ab	(1082)	-----RVAKMIERCYTALQCIRGAMGDVGLCMYRLK			
Murine hepatitis pol 1ab	(1304)	SFSMSPEETAQLYGSGITPNVCFVKGDIKVVRLVNAEV			
Consensus (1327)		SFSMSPEETAQLYGSCYTPNVCFVKGDIKVLKLVKAEV			
Section 36					
	(1366)	1366	1380	1390	1404
avian infectious bronchitis pol 1ab	(1039)	IVNAANEHNTHGSGVAKAIADFCCLDPEYCEDYVKKH			
bovine coronavirus pol 1ab	(1296)	VVNPNANGMAHGGVAKAIAVAAGQOEVKETTDMMVKSRG			
Human corona 229E pol 1ab	(1114)	DLHTGEMVMDYKCSCTSGRLEESAVLFCFTPTTKAFPY			
Murine hepatitis pol 1ab	(1343)	IVNPNANGMAHGGVAGATAEKA SAFTKETSDMMVKRAGG			
Consensus (1366)		IVNPNANGMAHGGVAKAIAE AGA FVKETTDMMVKAHG			



**FIGURE 4A (contd.)**

Section 37					
	(1405)	1405	1410	1420	1430 1443
avian infectious bronchitis pol 1ab (1078)	PQQR	-----	-----	-----	-----
bovine coronavirus pol 1ab (1335)	VGATGDCYVS	TGGKLCRTVLNV	VGPDARTQ	GKOSYALLE	
Human corona 229E pol 1ab (1153)	TCLNCNAPRMCT	TIROLOGTHIF	VQQRPEP	-----	VNP
Murine hepatitis pol 1ab (1382)	VCQVGEQYES	SAGGKLCKKVLN	IVGPDARG	HGKQCYSLLE	
Consensus (1405)	VCQ	GDCY S	GGKLC	VLNIVGPDAR	GKQ YALLE
Section 38					
	(1444)	1444	1450	1460	1470 1482
avian infectious bronchitis pol 1ab (1082)	-----	-----	-----	-----	-----
bovine coronavirus pol 1ab (1374)	RVYKHLNKYD	CVVTTETSA	GFESVPS	DMVSLTYLL	GGTAEK
Human corona 229E pol 1ab (1185)	VSEVVKPVCS	SIFRGAVSC	SHYQNIY	SONLCVDG	FGFVN
Murine hepatitis pol 1ab (1421)	RAYQHINKCD	NVVTNLTSA	GFESVPTD	VSITTYLL	CGVTK
Consensus (1444)	RAY	HINKCD	VVTTLIS	AGIFSVPS	DMVSLTYLLG L K
Section 39					
	(1483)	1483	1490	1500	1510 1521
avian infectious bronchitis pol 1ab (1110)	KLVAAYKNVL	VDGVMNYV	VPVLSL	GIFGVDF	KMSTDAMR
bovine coronavirus pol 1ab (1413)	QVVLVSNNQ	EDFDLISK	QITAVE	GTAKLAER	LSFNVGR
Human corona 229E pol 1ab (1224)	KEQPWTN	-----	DALNTIC	IKDADYNA	VEISVPIK
Murine hepatitis pol 1ab (1460)	NVTLVSNNO	DDFDVTR	COVTSV	AGTKA	SLALAKNICR
Consensus (1483)	KVVLVS	NNQDDFDVIA	KCQITL	VDGTKAL	ALKLSINLIR
Section 40					
	(1522)	1522	1530	1540	1550 1560
avian infectious bronchitis pol 1ab (1149)	EAFEGCTIR	VLLFS	-----	-----	-----
bovine coronavirus pol 1ab (1452)	SLVYETDANK	LILSNDVA	EVSTENV	LDDVLSLR	HDIALD
Human corona 229E pol 1ab (1256)	NTVDTTPKE	FPVKE	LNALFL	HDNVAFY	QGDVDTMVNC
Murine hepatitis pol 1ab (1499)	DVKFVTNAC	SSLES	ESCEVSS	YDVLOE	VEALRHDIQLD
Consensus (1522)	DIVF T A	LLFS DL	EVSSH	DVLQDV	ALRHDI LD
Section 41					
	(1561)	1561	1570	1580	1599
avian infectious bronchitis pol 1ab (1163)	-----	-----	-----	-----	-----
bovine coronavirus pol 1ab (1491)	DDARTEVQ	SNVDVMP	EGWRV	VNKEFYQ	INGVRTVKYEECP
Human corona 229E pol 1ab (1295)	VDFDFLV	NAANENLA	HGGGDA	KALDVY	TGKQLQRLSKEH
Murine hepatitis pol 1ab (1537)	DDARVEVQ	ANMDCLPT	WRVLN	KFDSV	DGVRTIKYEECP
Consensus (1561)	DDAR	EVQANMD LP	GWRLV	NKFD I	GVRTIKYEECP
Section 42					
	(1600)	1600	1610	1620	1638
avian infectious bronchitis pol 1ab (1163)	--LSQEHID	-----	-----	YFD--VT	CKOKTLY
bovine coronavirus pol 1ab (1530)	GGTILCS	QDKVEGY	VQOGSE	NKATVAQ	IKALFLDKVDIT
Human corona 229E pol 1ab (1334)	IGLAG	-----	-----	KVKVGT	GVMVECD
Murine hepatitis pol 1ab (1576)	GGIFVSS	QKKEGY	VONGSP	KEASVS	OIRALLANKVDVL
Consensus (1600)	GGIAI	SQDK FGY	VQNGSEK	ATVAQ	IKALS

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**FIGURE 4A (contd.)**

Section 43						
	(1639)	1639	1650	1660	1677	
avian infectious bronchitis pol 1ab (1182)		LTREDEVKYSIVLKP	GD SLGQFG	-----	QVYAKN	
bovine coronavirus pol 1ab (1569)		LTVDGVNFTNREVPV	GESEFGKSLGNV	EC DG	VNVTKHRC	
Human corona 229E pol 1ab (1360)		GPRKCKHERDLLPKAYNTINNEQ	GTPTLPIT	SCGIFGIK		
Murine hepatitis pol 1ab (1615)		CTVDGVNFRS	CCVAEGEVEFGKTLGS	VFCDG	INVTKVRC	
Consensus (1639)		LTVDGVNFRSILVK	GESF	GKSLGSVFCDGINVT	KHKC	
Section 44						
	(1678)	1678	1690	1700	1716	
avian infectious bronchitis pol 1ab (1211)		KIVFTADDVEDKELLYVPTTDKS	ILEY	GLDAQKYVIYL		
bovine coronavirus pol 1ab (1608)		INXKGRVEEEDNLSS	EDLKAVRSS	ENEDQKEL	LAYYNN	
Human corona 229E pol 1ab (1399)		LETSLEVLIDVCNTRKVRMFVYTD	TEVCKVKD	FV	SGLVN	
Murine hepatitis pol 1ab (1654)		ATYKGVSEFQMS	DLSPADLVAVKDAEG	DEP	DLKYTM	
Consensus (1678)		IIYKGVFFQF	NLSEVDL	AVSDSF	FDKDLLAYY M	
Section 45						
	(1717)	1717	1730	1740	1755	
avian infectious bronchitis pol 1ab (1250)		QTLAQKWNVOYRDNELILEWRD	GNCWISSAIV	LLQAAKT		
bovine coronavirus pol 1ab (1647)		LVNCSKRWQVVEFGKYFTEKQANN	NCFVNV	SCLMLQSLNL		
Human corona 229E pol 1ab (1438)		VQKVEQPKTEPK-PVSMIKVAPK	PYRMDGKFS	YETEDLL		
Murine hepatitis pol 1ab (1693)		LG-MCKW	SVVCGNYFAEK	SNNGYIN	VACLMLQHTSL	
Consensus (1717)		L M KWNV	VFKGN	YFIFKQANN	NCFINVACLMLQAL L	
Section 46						
	(1756)	1756	1770	1780	1794	
avian infectious bronchitis pol 1ab (1289)		RKKGELTEAWAKLLG-GDRT	DEVAWCY	SCTAKVG	DFSD	
bovine coronavirus pol 1ab (1686)		KEKIVQWQEA	WLEFRSGRPAREV	SLVL KGGFK	EGDPA	
Human corona 229E pol 1ab (1476)		CVADDKPIVLE	TD SMLTLD	DRGLALDN	LSGVLSAAIK	
Murine hepatitis pol 1ab (1731)		KEPKWQWQEA	WNEFRSGKPL	REVSLVL K	SEKENEPS	
Consensus (1756)		KFK FQWQEA	WFRSGKP	REVALVLAKGGFK	EGDPSD	
Section 47						
	(1795)	1795	1800	1810	1820	1833
avian infectious bronchitis pol 1ab (1327)		ANWLLANLAEHFDADYTNAFL	KRRVS	NCGIKS	-----	
bovine coronavirus pol 1ab (1725)		SRDFLRVVF	SQVDLTGAICD	FEI	ACKGVKQ	EQRTGVDA
Human corona 229E pol 1ab (1515)		QVDINKAIP-SG	LIKFDIGSVVVY	MVVPSE	--	KDKHL
Murine hepatitis pol 1ab (1770)		SIDIMRVVL	READLSGAT	NI	EFVCK	GVKQEQRKGVDA
Consensus (1795)		SIDFLRVV	ADLSGA	C	LEIVCKCGVKQEQRKGVDA	
Section 48						
	(1834)	1834	1840	1850	1860	1872
avian infectious bronchitis pol 1ab (1360)		--YELRG--	--LEACIQPV	RATNLLHFK	TQYSN	CPTCGA
bovine coronavirus pol 1ab (1764)		VMHFGT	LSREDLEIGY	TVDCSCG	KLIHCVR	EDVPFLIC
Human corona 229E pol 1ab (1551)		DNNVQR	CTRKLNR	LMCDIVCTIP	ADYLLPLV	LSLTCNV
Murine hepatitis pol 1ab (1809)		VMHFGT	LLKGD	LVRCYNTACTCGSK	LVHCTQ	ENVPFILIC
Consensus (1834)		VMHFGT	LSR DLEIGY	NIVCTCGAKLIHCL	ENVPTLIC	

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**FIGURE 4A (contd.)**

Section 49						
	(1873)	1873	1880	1890	1900	1911
avian infectious bronchitis pol 1ab (1393)	NN	DD	EMIEASLPYELL	FATD	GCPATMDCDE	DAVGTVVFMG
bovine coronavirus pol 1ab (1803)	SNT	PASVKKLR	KGXGSANL	FKGDKVGHYVHV	KCEQSYQLY	
Human corona 229E pol 1ab (1590)	SFV	GELKAAEAKV	LTIKVTEDG	VNMHDVTV	TDKSE	EQQ
Murine hepatitis pol 1ab (1848)	SNT	PEGRKLEDD	VVAANTFTGGS	SVGHYTHVKC	KPKYQLY	
Consensus (1873)	SNT	PELRKLP	VISANITDGG	AVVHVHV	KCD	SYQLY
Section 50						
	(1912)	1912	1920	1930	1940	1950
avian infectious bronchitis pol 1ab (1432)	STNS	GHCYTC	AAGQAFON	LAKDRKFG	KKSPYIT	PAMYTRF
bovine coronavirus pol 1ab (1842)	DASN	VKKVTD	VTEENLSDG	LYLKNLKQTE	KSVLTT	TYLLDD
Human corona 229E pol 1ab (1629)	VGVI	ADKDKDL	SSAMP	SDINTSEL	LTKAID	VDWVEFYGE
Murine hepatitis pol 1ab (1887)	DACN	VNVKVS	EAFONTD	G	LYLKNLKQTE	SSVLTTFYLLDD
Consensus (1912)	DA	NV	KVTDASGNLSD	CLYLKNLKQTE	SSVLTTFY	LD
Section 51						
	(1951)	1951	1960	1970	1989	
avian infectious bronchitis pol 1ab (1471)	AFK	NETSLP	VAKQSKG	SKSVKED	VSNLAT	SSKASFON
bovine coronavirus pol 1ab (1881)	VKK	LEVYN	EDLSQYY	CDGCKYYT	QRI	LKAEKTEFEKVDGV
Human corona 229E pol 1ab (1668)	KDA	VTPA	VDHSA	EAYESAV	VNGIR	VLKTSNNCWNNAV
Murine hepatitis pol 1ab (1926)	VKC	VEY	KPDI	SOYYCES	CKYYTK	PIIKRAQERTFEKVDGV
Consensus (1951)	VKK	VEYAPDLSQYY	CD	SKYYT	I	LKAEKTEFEKVDGV
Section 52						
	(1990)	1990	2000	2010	2028	
avian infectious bronchitis pol 1ab (1510)	TDFE	QWYDSN	IYESL	KVQESP	DNFDKY	VSEFTTKREDSKLP
bovine coronavirus pol 1ab (1920)	YTNE	K	LIGHTIC	DI	LN	AKLGEDSSKEEFYKVTWPTAT
Human corona 229E pol 1ab (1707)	CIAL	QYSKPH	FISQGL	DAAWN	KFVLGD	EIFVAFVYYVA
Murine hepatitis pol 1ab (1965)	YTNE	KLVGH	SIAEK	LN	AKLGED	CNSPEFYKVTWPTAT
Consensus (1990)	YTNE	FQLIGH	SI	E	LN	AKLGEDFVEYKVTWPTAT
Section 53						
	(2029)	2029	2040	2050	2067	
avian infectious bronchitis pol 1ab (1549)	LTE	KVRC	IKSV	DFRSK	GGFI	YKLTPTD
bovine coronavirus pol 1ab (1959)	GDV	VLAT	DDLY	VKRY	ERG	CITFGKPV
Human corona 229E pol 1ab (1746)	RLM	KGDK	DAED	LT	KL	SKYLANEAQV
Murine hepatitis pol 1ab (2004)	GDV	VLAS	DDLY	VSRYS	GG	CITFGKPV
Consensus (2029)	GDV	VLAS	DDLY	VSRYSKGC	ITFGKPV	VWLEHEASL
Section 54						
	(2068)	2068	2080	2090	2106	
avian infectious bronchitis pol 1ab (1588)	VLD	AIS	IKATW	VEGN	ANF	VGH
bovine coronavirus pol 1ab (1998)	TYF	NR	PL	LDEN	KFD	V
Human corona 229E pol 1ab (1785)	AKF	EN	SV	AS	ENSA	IVCAS
Murine hepatitis pol 1ab (2043)	TYF	NR	PS	V	CEN	KFN
Consensus (2068)	TYF	NR	SL	LV	EN	KFN

**FIGURE 4A (contd.)**

Section 55						
	(2107)	2107	2120	2130	2145	
avian infectious bronchitis pol 1ab (1615)		-----			KSLHI	
bovine coronavirus pol 1ab (2024)		-----			DISESDAKES	
Human corona 229E pol 1ab (1812)		-----			YCVHG	
Murine hepatitis pol 1ab (2082)		PGADASAGAGIAKEQKACASASVEDQVVTEVRQEPSVSA				
Consensus (2107)				DI	SVHA	
Section 56						
	(2146)	2146	2160	2170	2184	
avian infectious bronchitis pol 1ab (1620)		PTFWENAENFVKMGDKIGGVIMGLWRASHLNKPNLERTF				
bovine coronavirus pol 1ab (2034)		KEINIEKTSGVKKKFKVEDSVLVNDDTSEIKYVKSLSTV				
Human corona 229E pol 1ab (1817)		--IKYYSRVRSVRGRATIVSMEQLEPCAOSRLLESQVAYT				
Murine hepatitis pol 1ab (2121)		ADVKEVKLNGVKKPKVKEGSAVNDPTSETKVKVKSLSIV				
Consensus (2146)		DIKEIKLNGVKKP	KIEGSAVIVNDPTSESKLVKSLSIV			
Section 57						
	(2185)	2185	2190	2200	2210	2223
avian infectious bronchitis pol 1ab (1659)		NTAKKAIVSSVTTTQCGKLIGKAAIFIADKVGGGVMRN				
bovine coronavirus pol 1ab (2073)		DVYDMWLTGCRYVVRTANALSMANVPTLRKFKLKEGMITL				
Human corona 229E pol 1ab (1854)		AFSGPVDKGHYTYDTAKKSMYDGDREVKHDLSSLVMTS				
Murine hepatitis pol 1ab (2160)		DVYDMELTGCKYVWTANELSRLVNSPTREYVKWGKKGK				
Consensus (2185)		DVYDMELTGCKYVV	TANKLS	VNSPTIRKVIKFGVT		
Section 58						
	(2224)	2224	2230	2240	2250	2262
avian infectious bronchitis pol 1ab (1698)		ITDSLKGECGITRG-----				HFER
bovine coronavirus pol 1ab (2112)		VSLPFDLNLREIKPVENVVKAVERNKISACFNEFKWTFM				
Human corona 229E pol 1ab (1893)		VVMVGGYMAPVNTVKPKPMENQDDEKAQKFDEGDELTH				
Murine hepatitis pol 1ab (2199)		IVTPAKLLLRDEKQEVAPKVKAKATACYCAVKNFLI				
Consensus (2224)		IVIPIKLL	LRD K	F VIK VK KA	ACF	FIKWLIL
Section 59						
	(2263)	2263	2270	2280	2290	2301
avian infectious bronchitis pol 1ab (1716)		KMSPOFLKTIIMFFLFYFLKAS-----		VKS-----		V
bovine coronavirus pol 1ab (2151)		LLFGNKKISADNKVIYTTTEVASKLTCKLVALAEKNAFLT				
Human corona 229E pol 1ab (1932)		NEVIEFTWLLSMFTCKTAVTTGDDVKIMAKAPORTGVVL				
Murine hepatitis pol 1ab (2238)		YCESWIKENTDNKVIYTTTEVASKLTFRCCIAFKNALQT				
Consensus (2263)		LF	WIKFSLDNKVIYTTTEVASKLT	KL	LAFKNALLT	
Section 60						
	(2302)	2302	2310	2320	2330	2340
avian infectious bronchitis pol 1ab (1741)		VASYKEVLCKVVLATILLIVFVYTSNPVMTGIRVLDFL				
bovine coronavirus pol 1ab (2190)		EKWSVARGACTIATIELLINFNIYANVIFSDFYLPKIG				
Human corona 229E pol 1ab (1971)		KESLKYNLKASAAVLKSKWLLAKEIKLLELLIMTLYSVV				
Murine hepatitis pol 1ab (2277)		ENWSVSRGFPELVATVELLINFNIYANVILSDFYLPNIG				
Consensus (2302)		EKWSVARGA	IIATIFLLWFNFIYANVILSDFYLP	IG		

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**FIGURE 4A (contd.)**

Section 61					
	(2341)	2341	2350	2360	2379
avian infectious bronchitis pol 1ab (1780)		REGSLCCPYKDYG-----			KDSFDVLRVCA
bovine coronavirus pol 1ab (2229)		FLPTEVCKIAQMIKSTFSLVTICDLYSICDVGEKNOYCN			
Human corona 229E pol 1ab (2010)		LLCVRF---PEN---FCSETVN--GYAKSNEVKDDYCD			
Murine hepatitis pol 1ab (2316)		PLPTEVCGQIVAFKTTTEGVSTICDFYQVTDLGGYRSSECN			
Consensus (2341)		FLPTEVG I W KSTF L TICD Y IKDLGEK YCN			
Section 62					
	(2380)	2380	2390	2400	2418
avian infectious bronchitis pol 1ab (1804)		DDEICRVGLHDKDSARLYKHAYSNEQVYKDAASGFIENW			
bovine coronavirus pol 1ab (2268)		GSLAIOFCLAGEDMDNYKATDVQYHEADRRAFVDYTGVM			
Human corona 229E pol 1ab (2041)		GSLGCKMCLFGYQELSORHLIDVVKHBTDPFFSNMQPF			
Murine hepatitis pol 1ab (2355)		GSMVCELCFSGEDMDNYDAINVMQHVVDRRLSFDYISL			
Consensus (2380)		GSIIICKLCLAGFDMLDNYKHIDVVQHVDRRLS DY V			
Section 63					
	(2419)	2419	2430	2440	2457
avian infectious bronchitis pol 1ab (1843)		NWLYIVFLLLEVKPVAG-----FVLT--TCYCVKYLVLN			
bovine coronavirus pol 1ab (2307)		KKRVGEEIMSYALTAWFYPLAIESHQSLLTWLPELFM			
Human corona 229E pol 1ab (2080)		IVMVLLLEIFG-----DNYTRCFLLYEVAQMIS			
Murine hepatitis pol 1ab (2394)		FKLVVRLVIEGYSLYTVCFYPLEVLIGMOLLTWLPELFM			
Consensus (2419)		IKLVLELIIGYALYTA FYPLF LIIIQILTTWLPELFM			
Section 64					
	(2458)	2458	2470	2480	2496
avian infectious bronchitis pol 1ab (1874)		STVLQTVGVCFLDMEVQTMFSHFNFMGAGFYFWETFKYYT			
bovine coronavirus pol 1ab (2346)		LSTLHWSVRLLEVSLANMLPAHVFMRFYITLASFKLFIIL			
Human corona 229E pol 1ab (2107)		TVGMFLGSYKETNWEHLFIIRFDVICDELEVTVIVIKVVISF			
Murine hepatitis pol 1ab (2433)		LETMNSARLFEVEVANMLPAETLEERYEVVTAMYKVYCL			
Consensus (2458)		LSTLHWSVRLLEVWFANMLPAHVILRFYIVI ALIKVI L			
Section 65					
	(2497)	2497	2510	2520	2535
avian infectious bronchitis pol 1ab (1913)		QVAHLLYCKDVTCEVQKRVARSNRQEVSVVVGGRKQIVH			
bovine coronavirus pol 1ab (2385)		FRHVAYGCSKPGCLFYKRNRSRLRVKCSITIGCMIRYYD			
Human corona 229E pol 1ab (2146)		VRIVLEGUENEDCTACSKSARLKRFPMNTIANGVQRSEY			
Murine hepatitis pol 1ab (2472)		CRHVMYGCSKPGCLFYKRNRSRLRVKCSITVAGSLRYYD			
Consensus (2497)		RHVIYGCSKPGCLFCYKRNRSRLRVKVSTIVGGMIRYYD			
Section 66					
	(2536)	2536	2550	2560	2574
avian infectious bronchitis pol 1ab (1952)		MYTNSCYNECKRNNWYCRNCDDYGHQNTMSPFVAGEIS			
bovine coronavirus pol 1ab (2424)		VMANGGTGFCCKHOWNLDCDSYKRGNTFITVAAADLS			
Human corona 229E pol 1ab (2185)		VMANGGSKCKKHREFFVDEDSYGYGSCFITPVSREIG			
Murine hepatitis pol 1ab (2511)		VMANGGTGFCCKHOWNLNCNSWKPGNTFITHEAAADLS			
Consensus (2536)		VMANGGTGFCCKKHQWNCINCDSYKPGNTFITPEVAADLS			

**FIGURE 4A (contd.)**

Section 67					
	(2575)	2575	2580	2590	2600 2613
avian infectious bronchitis pol 1ab (1991)		EKLKRHV	PTAYAYHV	DEACLV	DEVNKYKAATPGKD
bovine coronavirus pol 1ab (2463)		KELKRPIQL	HDVAIHTV	TDVKQVGCYMR	EYERDGGORTY
Human corona 229E pol 1ab (2224)		NIT	TNVQPTG	PAEVMEDKVEFENG	EYRIYSCETFWRYN
Murine hepatitis pol 1ab (2550)		KELKRFPVN	PTDSAYYSV	TEVKQVGC	SMRLFYERDGGORVY
Consensus (2575)		KELKRVPQPTD	AYHTVTEVKQVGC	CFMRLFYERDGGOR Y	
Section 68					
	(2614)	2614	2620	2630	2640 2652
avian infectious bronchitis pol 1ab (2030)		SASSAVKCF	SVTDELEK	AVFLKEALCK	CEQDSNOGFIVCN
bovine coronavirus pol 1ab (2502)		DDVNASL	FVDYSNEL	LHSAKVGVP	MHVVVVEND
Human corona 229E pol 1ab (2263)		FDIT	ESKYSCKEV	FKN---CNV	LDDFLMFNNMG
Murine hepatitis pol 1ab (2589)		DDVNASL	FVDMGLLH	SAKVGVP	BETHVVVVE
Consensus (2614)		DDVNASL	FVDMS LLHSAKVGVP	DLHVVVVEND	
Section 69					
	(2653)	2653	2660	2670	2680 2691
avian infectious bronchitis pol 1ab (2069)		TQSAHALE	SAKN	AIYYAGY	CKELLILDOAIEQ
bovine coronavirus pol 1ab (2535)		---	ADKANFLN	AVEYAQSL	FRILMVVDKN
Human corona 229E pol 1ab (2293)		---	TNVTQVKN	SVYES	LICRILKVDSE
Murine hepatitis pol 1ab (2622)		---	ADKAGE	GAVERA	SYREMLMVEKK
Consensus (2653)		---	ADKANFLN	AAVFYAQSL	CRPILMVVDK LITTLNVG
Section 70					
	(2692)	2692	2700	2710	2720 2730
avian infectious bronchitis pol 1ab (2108)		PVS-	KSVIDKVC	SISSISV	TAALN
bovine coronavirus pol 1ab (2570)		TSVT	ETMEDVYVDT	ELSMEDV	RKSLNAL
Human corona 229E pol 1ab (2328)		FNG-	VLHKAYIDV	LRNSEGK	DLN
Murine hepatitis pol 1ab (2657)		LSVSR	TMFDLYVDS	ILNVLDV	BAKSLTSFVNAAHNSLKE
Consensus (2692)		SVSKT	TMFDLYVDTLLS	IFDVDRKSLNA	I AH SIK
Section 71					
	(2731)	2731	2740	2750	2769
avian infectious bronchitis pol 1ab (2134)		---	YKAGTL	RDALLSIT	KDFAVDMALFCHN
bovine coronavirus pol 1ab (2609)		GTOT	CKVDETE	LSCAK	CSIDSVDTRCL
Human corona 229E pol 1ab (2352)		---	MSLA	CKRAL	GLSLSDHEFTS
Murine hepatitis pol 1ab (2696)		GVOLE	QVMDTE	LCARRK	CAIDSDVETK
Consensus (2731)		G QI	VLDTF	ISCARKKCAIDSDVDT	REITDSVMSAVN
Section 72					
	(2770)	2770	2780	2790	2808
avian infectious bronchitis pol 1ab (2162)		HDVDYT	CDCE	TNVLP	SXGIDTCKLTPR
bovine coronavirus pol 1ab (2648)		AGLE	TTDESCN	NLVPT	TRG-DNIVAA
Human corona 229E pol 1ab (2380)		CDVLL	SDLS	ENFVSS	AKPEEKESAY
Murine hepatitis pol 1ab (2735)		AGVD	TTDESCN	NLVPT	VKS-DTEVAADL
Consensus (2770)		AGVDLT	DESENNLVPSYK	DKIVAADL	LGVLION AKH

**FIGURE 4A (contd.)**

Section 73						
	(2809)	2809	2820	2830	2847	
avian infectious bronchitis pol 1ab (2201)		ANLRMKNAP--	EVVAKFSELIRL	DSCLKYLISATVKS		
bovine coronavirus pol 1ab (2686)		VOGNVAKIACV	SVDAFNQL	SDFOHKLKACCKTG		
Human corona 229E pol 1ab (2419)		VNANVLTKDQ	TRIVHAKDENSL	SAEGRKYIMKTSKAC		
Murine hepatitis pol 1ab (2773)		VOANVAKAANV	ACISVDAFNQL	SADLOHRLRKACSKTG		
Consensus (2809)		VNANVAKAANV	PCIWSVDAFNQLSAD	QKYLKAC	KTG	
Section 74						
	(2848)	2848	2860	2870	2886	
avian infectious bronchitis pol 1ab (2238)		VREFITKSGAKQ	VIACHTOKLLVEKKAG	GIVSGTFKCEK		
bovine coronavirus pol 1ab (2725)		LKLLKLTYNKQ--	MANVGLTTPESL	KGGAVES-----		
Human corona 229E pol 1ab (2458)		LTLLLTINENQ	AVTQIPATSIIVAKQ	GADAGH-----		
Murine hepatitis pol 1ab (2812)		LKIKLITYNKQ--	EANVPILTTTPFSL	KGGAVES-----		
Consensus (2848)		LKFKLTYNKQ	VANVPILTTTPFSL	KAGAVES		
Section 75						
	(2887)	2887	2900	2910	2925	
avian infectious bronchitis pol 1ab (2277)		SYFKWLLIF	YILETACCSGMY	YMEMSKSFVHPMY	OVNST	
bovine coronavirus pol 1ab (2755)		-----YFVY	VCFLLSHVCF	FIGEWCLMPT	YTVHKSD	
Human corona 229E pol 1ab (2490)		-----SLT	WLWLLCGLVCL	IQYLCFFMPY	FMYDIVSS	
Murine hepatitis pol 1ab (2842)		-----RMLQ	WLEVANITCE	IVLWLMPT	VAVHKSDMOL	
Consensus (2887)			ILYILFLA	LVCFI	LWLLMPTYHVMYSDMSL	
Section 76						
	(2926)	2926	2940	2950	2964	
avian infectious bronchitis pol 1ab (2316)		LHVEGEKVIDK	GVLRREIVPEDT	CFSKVNDAFWGRPY		
bovine coronavirus pol 1ab (2788)		PVYASYKVL	DNVIRDVSVEDV	CFANKFO	DQWYESTE	
Human corona 229E pol 1ab (2523)		PEGYDFY	ENQDKNFLAPLK	VRVVENEDWHYAKF		
Murine hepatitis pol 1ab (2875)		PLYASEK	VIDNVLRDVSVTDA	CFANKFO	DQWYESTE	
Consensus (2926)		PLYASEKVIDN	GVLRDVSVED	CFANKFENFDQWYESTE		
Section 77						
	(2965)	2965	2970	2980	2990	3003
avian infectious bronchitis pol 1ab (2355)		DNSRNCPIV	TAVIDGDGT	VATGVPGFVSWV	MDGVMFTHM	
bovine coronavirus pol 1ab (2827)		GLSYYSNSMA	----	CPIVVAVVDQ	DLGSTVFNVP	TKVLR
Human corona 229E pol 1ab (2562)		GFTPLNK-Q	----	SCPTVGV	SEIVNTVA	IPSNVYL
Murine hepatitis pol 1ab (2914)		GLAYYRNSKA	----	CPVVVAVIDQ	DIGHTL	FNVP
Consensus (2965)		GLSYYNSMA		CPIVVAVGVQ	DIVSTVFNVP	VLR
Section 78						
	(3004)	3004	3010	3020	3030	3042
avian infectious bronchitis pol 1ab (2394)		TQTERKPWYI	PTWFNREIVG	YTQDSITTEGSEFY	TSIALF	
bovine coronavirus pol 1ab (2862)		YGYHVLHFI	THAFADGVQ	CYTPHSQTS	YSNEYASGCVL	
Human corona 229E pol 1ab (2594)		VGKTLTPTL	QAAPNAGVCY	DIEGVTTPEK	-----CLF	
Murine hepatitis pol 1ab (2949)		YGFHVLHFI	THAFADSVOCY	TPHMOTPYD	NEYASGCVL	
Consensus (3004)		YGFHVLHFI	THAFANDGVQ	CYTPHSQIPY	NEYASGCVL	

**FIGURE 4A (contd.)**

Section 79					
	(3043)	3043	3050	3060	3070 3081
avian infectious bronchitis pol 1ab (2433)		SARCLYETASNTFPOLYCFNGDNDAP	ALPEG	SIIPHRV	
bovine coronavirus pol 1ab (2901)		SSACTMAMADGSPQPYCYTEGLMONASLYS	EMPHVR		
Human corona 229E pol 1ab (2627)		TSACTRLEGLGGN-NVYCYNTALMEGSLPYSSIQANAY			
Murine hepatitis pol 1ab (2988)		SSLTMTLAHADGTPHRYCYTCGVMMHNASLYSCLAPHVR			
Consensus (3043)		SSACTMLAAADGSPNPYCYTDGLM	NASPYSSIIPHVR		
Section 80					
	(3082)	3082	3090	3100	3110 3120
avian infectious bronchitis pol 1ab (2472)		FQPNG--VRLIVPQOILHTPYV	KFVSDSYGEGSVCEYT		
bovine coronavirus pol 1ab (2940)		NLANAKGFIRFPEVIREGLVRTV	RTRSMSCRVGLCEEA		
Human corona 229E pol 1ab (2665)		KYDNGNFIKLPEVTAQGFGRTRTIATK	CVGEVVE		
Murine hepatitis pol 1ab (3027)		NLAASNGYIRFPEVSEGLVRV	RTRSMTCRVGLCEEA		
Consensus (3082)		NLANGNGVIRFPEVL	EGIVRVVTRSMSCRVGLCEEA		
Section 81					
	(3121)	3121	3130	3140	3159
avian infectious bronchitis pol 1ab (2509)		RPGYCVSLNPQWLFNDENTSKP	VEFGSTVREIMF	SMV	
bovine coronavirus pol 1ab (2979)		DEICFENENGSWLNNDYRSLPCTFC	RDVFD	TYQL	
Human corona 229E pol 1ab (2704)		NAGVDEGDKWE	NDG---RVANCYV	GTGWN	VENIL
Murine hepatitis pol 1ab (3066)		EEICFENENRSWLNNPXYRAMP	TE	GRNAED	THOV
Consensus (3121)		DEGICFENKSWVLNNDYRSLPGTFCGR	VFDLIFQIL		
Section 82					
	(3160)	3160	3170	3180	3198
avian infectious bronchitis pol 1ab (2548)		STFEFGVNPN-TYMOLATMFLLV	VVVLTFAMV	KFCGV	
bovine coronavirus pol 1ab (3018)		KGLAOPVDFLALTASSIAGAILAV	VVVLVEYYLI	KLKRA	
Human corona 229E pol 1ab (2740)		SMESSFSVAAMSGOILLNCALGAF	ATCCELVT	KRRM	
Murine hepatitis pol 1ab (3105)		CGLVRPIDEFALTASSVAGALLAT	IVVDAFYLLI	KLKRA	
Consensus (3160)		SGLASPVDF	ALTASSIAGAILAVIVVLIFYYLIKLR		
Section 83					
	(3199)	3199	3210	3220	3237
avian infectious bronchitis pol 1ab (2586)		KAYATVPTMTLVVVTNAFLIC	THSYNSVLAVILLVLY		
bovine coronavirus pol 1ab (3057)		GDYTSIFVNVIWCV	FMMLF	EQVYPTLSCVYATCY	
Human corona 229E pol 1ab (2779)		GDLSVGCTVVVAVLL	NVSYINTONLV	MIAYAILYE	
Murine hepatitis pol 1ab (3144)		GDYTSMVVNVIWCV	ELMLF	EQVYPTLSCLYACEY	
Consensus (3199)		FGDYTSIVFINVIWCV	INFLMLFV	FQVYPTLSCIYAI	
Section 84					
	(3238)	3238	3250	3260	3276
avian infectious bronchitis pol 1ab (2625)		CYASTVTSRNTVIMHCWLV	FTFGLIVT	LACCYLGF	
bovine coronavirus pol 1ab (3096)		PYATLYPSEISVIMHLQWL	VMYGTIML	ECILLISVV	
Human corona 229E pol 1ab (2818)		FATRSRLR--YA-WIWCAAYLI	AYIS	AWLCAW	FLAM
Murine hepatitis pol 1ab (3183)		FYTTLYFPSEISVIMHLQWL	VMYGATIML	ECII	VAVV
Consensus (3238)		FYTTLYFPSEISVIMHLQWL	VMYGSIMPLWLCIIYIAV		



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**FIGURE 4A (contd.)**

Section 85				
	(3277)	3277	3290	3300 3315
avian infectious bronchitis pol 1ab (2664)		HYMYTPLFLWCYGTTRKNTKRYDGNFMCNMDLAAKS		
bovine coronavirus pol 1ab (3135)		VS-----NHAFWVFAYGRREGTCVRSDDTEEMALTT		
Human corona 229E pol 1ab (2854)		LTGL----LPSSLKLVSTNIFEGDKFVTFESAAGTF		
Murine hepatitis pol 1ab (3222)		VS-----NHALWLFKYCRKLGTVRSVGTFEEMALTT		
Consensus (3277)		VS	NHALWLFKYCRKLGTVRSVGTFEEMALTT	
Section 86				
	(3316)	3316	3330 3340	3354
avian infectious bronchitis pol 1ab (2703)		VIRGSEFVMTNEEG-DKFEAYLSAYARLKYYSGTGSEQ		
bovine coronavirus pol 1ab (3168)		MITKDSYCKLKNSISDVAENRYLSLNKYRYSEKMDTA		
Human corona 229E pol 1ab (2889)		VDMRSYERANSTISPEKLSAASNRYRYSEGNANEA		
Murine hepatitis pol 1ab (3255)		MITKESYCKLKNSISDVAENRYLSLNKYRESEKMDTA		
Consensus (3316)		MITKDSYCKLKNSISDVKFNRYLSLYNKYKYSGKMDTA		
Section 87				
	(3355)	3355 3360	3370 3380	3393
avian infectious bronchitis pol 1ab (2741)		DILQCRAWLYLDQYR-NSGVEIVTPRYSTGVRI		
bovine coronavirus pol 1ab (3207)		AIREAACSQLAKMDTFNNNGSDVLYQPTASVSTFL		
Human corona 229E pol 1ab (2928)		DRCQYAYLAKMLDFSRDHN-DILTPTVSYG-STL		
Murine hepatitis pol 1ab (3294)		AIREAACSQLAKMETENHNNGNDVLYQPTAVTTFEL		
Consensus (3355)		DYREACCAQLAKAMDTFS	NNG DILYTPPTASVGTSFL	
Section 88				
	(3394)	3394 3400	3410 3420	3432
avian infectious bronchitis pol 1ab (2779)		QSGFKLVSPSSA-KLISVSRGNMNGINIGIT		
bovine coronavirus pol 1ab (3246)		QSGIVMVSITSKPITSVTGNMILNGVLDIKVYC		
Human corona 229E pol 1ab (2965)		QALRMAQPSGFKVRCGNTVEMVWLGIV		
Murine hepatitis pol 1ab (3333)		QSGIVMVSITSKPITSVTGNMTKLTEDDKVYC		
Consensus (3394)		QSGIVKMVSPSSKVEFCIVSVTYGNMTLNGVLWLGDKVYC		
Section 89				
	(3433)	3433 3440	3450 3460	3471
avian infectious bronchitis pol 1ab (2818)		PRHVLGRFSGDOWNVNLNANNHEFEVTTQHG--VTNV		
bovine coronavirus pol 1ab (3285)		PRHVICSSADMTNPYTNLLCRVTSSDFTVLFRLSLTV		
Human corona 229E pol 1ab (3004)		PRHVIAASN-TTSAIPYDHEYSIMRLHNESITSGTAFGV		
Murine hepatitis pol 1ab (3372)		PRHVICSSADMTDPPXPNLICRVTSSEDFCVMSGRMSLT		
Consensus (3433)		PRHVICSASDMT PDY NLLCRVTSSDFTVISGRLSLTV		
Section 90				
	(3472)	3472 3480	3490 3500	3510
avian infectious bronchitis pol 1ab (2855)		VSRREKAVLLIQTAVANAEEKKYKIKANCCDSITAC		
bovine coronavirus pol 1ab (3324)		MSYQMQGMLVLTVTLQNSRTPKYTGCVVKPGETTVLA		
Human corona 229E pol 1ab (3042)		VCATMNVTKLIVSQTMHRRHSRTLKSEGENILA		
Murine hepatitis pol 1ab (3411)		MSYQMQGCLVLTVTLQNPNTKYSQGVVKPGETTVLA		
Consensus (3472)		MSYQMQGCMVLVLTVTLQNA	TPKYSFGVVKPGETFTILA	

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**FIGURE 4A (contd.)**

Section 91					
	(3511)	3511	3520	3530	3549
avian infectious bronchitis pol 1ab (2894)		AACGCTVVGLYPTMTMSNGTIRASFLAGACGAVGPNLEKG			
bovine coronavirus pol 1ab (3363)		ATNGKPGQAFHVMTMSSTYTIKGSFLCGSACGSGVGYVLMGD			
Human corona 229E pol 1ab (3081)		CYDGCAGQVPGVNMRTNWTTRGSPINCACGSPSYNLKNG			
Murine hepatitis pol 1ab (3450)		AYNGRPQGAFFHTLRSSTHTIKGSFLCGSACGSGVGYVLTGD			
Consensus (3511)		AYNGKPGQAFHVMTMRSSWTIKGSFLCGACGSGVGYVL			GG
Section 92					
	(3550)	3550	3560	3570	3588
avian infectious bronchitis pol 1ab (2933)		VVNFYFMHLELPNALHTGTDLMEFFYGGYVDEEVAQRV			
bovine coronavirus pol 1ab (3402)		CVKRVYMHQLEELSTGCHTGTDFENODFACPYKDAQVVQLP			
Human corona 229E pol 1ab (3120)		EVEFVYMHQLEELSGSGSHVGSSEDEVMTCGHEHQPNIDVE			
Murine hepatitis pol 1ab (3489)		SVRFVYMHQLEELSTGCHTGTDESCHFYGPYKDAQVVQLP			
Consensus (3550)		VKEFVYMHQLEELSTGCHTGTDF		GDFYGPYKDAQVVQLP	
Section 93					
	(3589)	3589	3600	3610	3627
avian infectious bronchitis pol 1ab (2972)		PPDNIVTNNIVAWLFAHLSVKESSFSLPKWLESTTVSV			
bovine coronavirus pol 1ab (3441)		VQDYIQSVFAWLYAAILNN-----CNWFEVQSDKCSV			
Human corona 229E pol 1ab (3159)		SANQMLTVVAFLAAILNG-----CPWLLKGEKLFV			
Murine hepatitis pol 1ab (3528)		VQDYTOTVAVWLYAAILNR-----CNWFEVQSDSCSE			
Consensus (3589)		VQDYIQTVNVVAVWLYAAILN			CNWFLQSDKCSV
Section 94					
	(3628)	3628	3640	3650	3666
avian infectious bronchitis pol 1ab (3011)		DDYAKNAGNGETTPSTGTATKLSAITSVDVCKLIRTD			
bovine coronavirus pol 1ab (3474)		EDFNVAWLSNGTSQVKSDELVDALASMECSLETLLAAI			
Human corona 229E pol 1ab (3192)		EHYNERAQAQNTAMNGEDAFSILAAKTCVERLLHA			
Murine hepatitis pol 1ab (3561)		EEFNVAWLSNGTSSTIKADLVLDALASMTVEQVTA			
Consensus (3628)		EDFNVAWLSNGFSAIKADLVLDALAAMTGVSVEKLLAAI			
Section 95					
	(3667)	3667	3680	3690	3705
avian infectious bronchitis pol 1ab (3050)		MYKNSQWGGDPETHQYNFEDEETPESVENIGGVRSQS-			
bovine coronavirus pol 1ab (3513)		KRLKNGEQQRQIMGSCSEDELTPSDVYQQLAGVKLQSK			
Human corona 229E pol 1ab (3231)		QMLNNGGEGKQILSYSSLEHDEFISINEVKKMFVNVLS-			
Murine hepatitis pol 1ab (3600)		KRLKSGEQQRQILSCVLEDELTPSDVYQQLAGVKLQSK			
Consensus (3667)		KVLNSGFGQKQILGSCSLEDELTPSDVYQQLAGVKLQSK			
Section 96					
	(3706)	3706	3720	3730	3744
avian infectious bronchitis pol 1ab (3088)		-SFVRKATIS-WWSRCVLAECFVLCIAIVLFTAVPLKEY			
bovine coronavirus pol 1ab (3552)		RTRIVKGIVCWIMASTELFCSTIAFVRWTFMFMYVTNM			
Human corona 229E pol 1ab (3269)		-GKTSMFKSISLFAGEFVMEWALLEVYTUTLWVNGFL			
Murine hepatitis pol 1ab (3639)		RTRVIKGTCCWILASTELFCSTIAFVRWTFMFMYVTNM			
Consensus (3706)		RTRVIKGT	CWILASTELFCFIISL	FVRWTFMFMYVTNM	

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**FIGURE 4A (contd.)**

Section 97					
	(3745)	3745	3750	3760	3770 3783
avian infectious bronchitis pol 1ab (3125)		MYAAMILLMAVLEISFTV	GVMAVMDTEHPTLTITVIG		
bovine coronavirus pol 1ab (3591)		LSITFCALCVISLAMDIV	HKHLYLTMYITLVLTTLEYN		
Human corona 229E pol 1ab (3307)		TPFMILLVALSLCLTFVVR	KKVLEDOVFLLPSIIVAATQ		
Murine hepatitis pol 1ab (3678)		EGVTLCALCTVSEFAMLLT	KKHLYLTMYIMPVLCTLFY		
Consensus (3745)		LITICLLCLVSEFAMLLV	KKHLYLTMFILPVLITLIYN		
Section 98					
	(3784)	3784	3790	3800	3810 3822
avian infectious bronchitis pol 1ab (3164)		VCAEVPFIYNTLISQVV	IFLSQWYDPVVEDTMVPWMFLP		
bovine coronavirus pol 1ab (3630)		NYLVVYKQTERRGYVYAW	LSVYVPSVEYTYTDEVTYGMLL		
Human corona 229E pol 1ab (3346)		NCAWDYHVTKVLAEKFDYN	VSVMOMDIQGFVNIFICLFM		
Murine hepatitis pol 1ab (3717)		NYLVVYKQSERGAYAW	LSHFVPAVDYTYMDEVTYGVVL		
Consensus (3784)		NYLVVYKQTERLIAYAW	LSVSVPAVDYTYDEVIYGLLL		
Section 99					
	(3823)	3823	3830	3840	3850 3861
avian infectious bronchitis pol 1ab (3203)		LVTDTAFKCVQGCYMNSFNT	SLLMIXOFVKLGFLVYITSS		
bovine coronavirus pol 1ab (3669)		LTGMVFVTLRSINHD	-----	LFSEIMVGRVISVV	
Human corona 229E pol 1ab (3385)		ALLHTWRFAKER	-----	CTHWCTYBFSLL	
Murine hepatitis pol 1ab (3756)		LIVAMVFVIMRSINHD	-----	VFSYMFVGRVLSLV	
Consensus (3823)		LVLNVFVTLRSINHD		LFSEI LVGRVLSLV	
Section 100					
	(3862)	3862	3870	3880	3890 3900
avian infectious bronchitis pol 1ab (3242)		NULTAYTGHWELFEVHTTV	LANVSSNSLIGLFVFKC		
bovine coronavirus pol 1ab (3699)		SLWYMGSNLEEEILLMLAS	SLFGTYTWTTLASMAAAKVIA		
Human corona 229E pol 1ab (3409)		AVLYTALYSYDYMSLLVML	LCAISNEWYTGALIFRICRF		
Murine hepatitis pol 1ab (3786)		SNWYFGANLEEEVLLPLT	SLFGTYTWTTLMSIATAKVIA		
Consensus (3862)		SLWY GSNLEEEVLLLL	MSLFGTYTWTTLISIA AKVIA		
Section 101					
	(3901)	3901	3910	3920	3939
avian infectious bronchitis pol 1ab (3281)		AKWMLYYCNAVLYLNHYVI	MAVMVNCIGWLCCTCFGLYWN		
bovine coronavirus pol 1ab (3738)		KWVAVNVLYETDIPQIKLV	LCYLFICYTISCYWGFLFSL		
Human corona 229E pol 1ab (3448)		GVAFLPVEVVSIFDGVKT	VLLFYMLLFVSCMYLLYW		
Murine hepatitis pol 1ab (3825)		KWLAVNVLYETDVPQIKLV	LLSYLCTGYVCCGYNCTLSL		
Consensus (3901)		KWLALNVLYFTYIPQIK	LVLL YLCIGYVCCCYWGLLSW		
Section 102					
	(3940)	3940	3950	3960	3978
avian infectious bronchitis pol 1ab (3320)		VHKVEGLTLCKYNEKVSVD	QYRIMCLHKEHPPKTVWEVF		
bovine coronavirus pol 1ab (3777)		MNSIERMPLGVVNYKT	VQELRYMNANGLRPPKNSFEAL		
Human corona 229E pol 1ab (3487)		INRCKCTGVVDECV	PAEFKIVANGLNAENGPEDAL		
Murine hepatitis pol 1ab (3864)		INSIERMPLGVVNYKT	VQELRYMNANGLRPPKNSFEAL		
Consensus (3940)		INSIERMTLGVVNFKIS	VQELRYMNANGLRPPKNSFEAL		

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**FIGURE 4A (contd.)**

Section 103						
	(3979)	3979	3990	4000	4017	
avian infectious bronchitis pol 1ab (3359)	STN	ILTQSLGG	DRVLPPTATV	AKESDVKCTTVVLMQLLT		
bovine coronavirus pol 1ab (3816)	MLN	FKLLIGGG	VPTTEVSQFQ	SKLTDVVKCANVVLINCGQ		
Human corona 229E pol 1ab (3526)	FLS	EKLMIGGP	RTIRVSTV	ESKLTDLCTNNVLMCILS		
Murine hepatitis pol 1ab (3903)	MLN	EKLLGGG	VPTTEVSQFQ	SKLTDVVKCANVVLINCGQ		
Consensus (3979)	MLN	EKLLGIGG	VRVIEVSTV	QSKLTDVVKCTNVVLLNCLQ		
Section 104						
	(4018)	4018	4030	4040	4056	
avian infectious bronchitis pol 1ab (3398)	HLN	VEANERK	MHVTLVELH	NKTLASDLVGECDNLEGLLI		
bovine coronavirus pol 1ab (3855)	HLH	VASNSK	LWQYCSILLNE	LATSDLGVAFEKIAQLLI		
Human corona 229E pol 1ab (3565)	NMN	TASLSEK	WAYCMEMENK	LNLCDDPETAQELLTAALTA		
Murine hepatitis pol 1ab (3942)	HLH	VASNSK	LWQYCSILLNE	LATSDLGVAFEKIAQLLI		
Consensus (4018)	HLN	VIASNSK	LWQYCVTLH	NKILATSDLGVAFDKLLQLLI		
Section 105						
	(4057)	4057	4070	4080	4095	
avian infectious bronchitis pol 1ab (3437)	TLE	CIDSTED	-----	TSLEYCDDITKRSTV	OSVTOEES	
bovine coronavirus pol 1ab (3894)	VLE	FANPAAVDS	SKGLTSTEEVC	DDYAKDNTVLQALQSEFV		
Human corona 229E pol 1ab (3604)	FEL	SKHSDFG	-----	LGDLVSYFENDST	OSVASSIV	
Murine hepatitis pol 1ab (3981)	VLE	FANPAAVDS	SKGLTSTEEVC	DDYVRDNTVLQALQSEFV		
Consensus (4057)	VLE	FANPAAVDS	SKCLSIEEVC	DDYLKDNTVLQALQSEFV		
Section 106						
	(4096)	4096	4110	4120	4134	
avian infectious bronchitis pol 1ab (3470)	HET	PYAEYTRAK	NLYKVLVDSK	NGGVTOQELAAAYKKA		
bovine coronavirus pol 1ab (3933)	NMA	SFVEYELAK	KNLDEAKASGSAN	---QQQIKOLEKAC		
Human corona 229E pol 1ab (3637)	GMP	SEVAYETRO	FYENAVANGSS	---PQITKOLEKAC		
Murine hepatitis pol 1ab (4020)	NMA	SFVEYELAK	KNLDEAKASGSAN	---QQQIKOLEKAC		
Consensus (4096)	NMP	SFVEYELAK	KNYDEARASGSAN	QQQIKOLEKAC		
Section 107						
	(4135)	4135	4140	4150	4160	4173
avian infectious bronchitis pol 1ab (3509)	NI	AKSVEFDRD	LAVQKKLDS	MAERAMT	TMETFAVTD	DRRA
bovine coronavirus pol 1ab (3969)	NI	AKSAYERD	RAVARKLERM	ADLALTN	MYKEAR	INDKKS
Human corona 229E pol 1ab (3672)	NV	AAEFDESS	VOKKLNREE	QAAAM	YELAVNR	KKS
Murine hepatitis pol 1ab (4056)	NI	AKSAYERD	RAVARKLERM	ADLALTN	MYKEAR	INDKKS
Consensus (4135)	NI	AKSAFDRD	RAVQKKLERM	ADLALTN	MYKEAR	INDKKS
Section 108						
	(4174)	4174	4180	4190	4200	4212
avian infectious bronchitis pol 1ab (3548)	KV	VSA	LQTLFSLR	KKLDNQALNSILD	NAVKGCVPLNAT	
bovine coronavirus pol 1ab (4008)	KV	VSA	LQTLFSLR	KKLDNQALNSILD	NAVKGCVPLNAT	
Human corona 229E pol 1ab (3711)	KV	VSA	LQTLFSLR	KKLDNQALNSILD	NAVKGCVPLNAT	
Murine hepatitis pol 1ab (4095)	KV	VSA	LQTLFSLR	KKLDNQALNSILD	NAVKGCVPLNAT	
Consensus (4174)	KVV	SA	LQTLFSLR	KKLDNQALNSILD	NAVKGCVPLNAT	

**FIGURE 4A (contd.)**

Section 109					
	(4213)	4213	4220	4230	4240 4251
avian infectious bronchitis pol 1ab (3587)		PIMCSNRLTLVLPDPETWVKCEGVLVYISTVVENIDTV			
bovine coronavirus pol 1ab (4047)		PSLAANTLTITVEDKSVYDQVVDNVYVTAGNVAQIQTI			
Human corona 229E pol 1ab (3750)		PATSAARIVVVVDHDSFVKMMVDGEVHYAGVWTTQEV			
Murine hepatitis pol 1ab (4134)		PSLTISNTLTITVEDKQVEDQVVDNVYVTAGNVWHIQFI			
Consensus (4213)		PSLSANTLTIIIVPDKDVFVQVVDNVYVTYAGVVWNIQTI			
Section 110					
	(4252)	4252	4260	4270	4280 4290
avian infectious bronchitis pol 1ab (3626)		TLADCTELHPTSTGSGLTTCISGANIAMPKMNITRNGH			
bovine coronavirus pol 1ab (4086)		QISDCTNKQLNELSD-----DCNWPVIAHRHNE			
Human corona 229E pol 1ab (3789)		KDNDGKKNVHLKDMTK-----ENQEI VWPITLTCE			
Murine hepatitis pol 1ab (4173)		QADGCAVKQLNETDV-----NSTWRPIVIAHRHNE			
Consensus (4252)		QDADGTNKQLNEIS			N NWPLVI LNRHNE
Section 111					
	(4291)	4291	4300	4310	4329
avian infectious bronchitis pol 1ab (3665)		NKMDVVLO--NIELMHGMRKTKACVAGVDAHGSVEISKCY			
bovine coronavirus pol 1ab (4116)		VSATVLO--NIELMAKLKTQVNS--GPDQTCNTPTQCY			
Human corona 229E pol 1ab (3819)		RVYKIQ--NIELTGKMKVKATKG--EGDGGITSEGNALY			
Murine hepatitis pol 1ab (4203)		VSTVVLO--NIELMEQKLRTOVNS--GSDMNCNTPRQCY			
Consensus (4291)		VSV VLQ NMELMPAKLKTQVNS G DA CNTPTQCY			
Section 112					
	(4330)	4330	4340	4350	4368
avian infectious bronchitis pol 1ab (3704)		TNISGNSVVAATSSNENDKVASFLNEA NQHYVDLDE			
bovine coronavirus pol 1ab (4153)		NNSNNGKIVYILSDVDGLKYTRILKDDNFVVLELDP			
Human corona 229E pol 1ab (3855)		NNEGGRAFMY YVETKPGMYVKWERDS--VVTVELE			
Murine hepatitis pol 1ab (4240)		NTTGTGKIVYILSDCDGLKYTRIVKED NCVVLELDP			
Consensus (4330)		NNSGGGKIVYAILSD PGLKYTKILKDDGN VVLELDP			
Section 113					
	(4369)	4369	4380	4390	4407
avian infectious bronchitis pol 1ab (3743)		CKREGMKVGKVFVYLYLNTRSTVRGMVLAISNVV			
bovine coronavirus pol 1ab (4192)		CKFTVQDVKGLKIKLYFVKGNTLAREWVQIFSSSTR			
Human corona 229E pol 1ab (3893)		CRFVLTPTGPQIKLYFVNLLNDRGAVLYIGATVR			
Murine hepatitis pol 1ab (4279)		CKFSVQDVKGLKIKLYFVKGNTLAREWVQIFSSSTR			
Consensus (4369)		CKFSVQDVKGLKIKLYFVKNCNTLARGVVLGTISSTR			
Section 114					
	(4408)	4408	4420	4430	4446
avian infectious bronchitis pol 1ab (3782)		LUSKGHELEEVDAVGTLSTSPAVDPAADTYCKYVAACNQ			
bovine coronavirus pol 1ab (4231)		LQAG-TATEYASNSAILSLCAFAVDPKKTYLDYIKQGG			
Human corona 229E pol 1ab (3932)		LQAG-KQTEVSNSHLTHCSAYPAALDAVKQAK			
Murine hepatitis pol 1ab (4318)		LQAG-TATEYASNSAILSLCAFAVDPKKTYLDYIKQGG			
Consensus (4408)		LQAG TATEYVSNAILSLCAFAVDPKKTYLDYIKQGG			

**FIGURE 4A (contd.)**

Section 115						
	(4447)	4447	4460	4470	4485	
avian infectious bronchitis pol 1ab (3821)		PLGNYVHMLTVHNCSEFALITSRKPTDDEPSVGGASVCH				
bovine coronavirus pol 1ab (4269)		PTANQYKMLCDHACTGMAITVKPDATTNQDSYGGASVCI				
Human corona 229E pol 1ab (3970)		PVGNOVKMLTNGSLSQQAITCTIDSNITTDITYGGASVCI				
Murine hepatitis pol 1ab (4356)		EVTNCGMLCDHACTGMAITLKPEATTNQDSYGGASVCI				
Consensus (4447)		PVGNCVKMLTDHAGSGMAITIKPDATTNQDSYGGASVCI				
Section 116						
	(4486)	4486	4500	4510	4524	
avian infectious bronchitis pol 1ab (3860)		YCRAHIAHNGSVGNLDGRGQFKGFTFQITTEKDPVCEC				
bovine coronavirus pol 1ab (4308)		YCRARVEHP-----DVDGLCKLRKRFVQVVGIGKDPVSYV				
Human corona 229E pol 1ab (4009)		YCRAHVAHF-----TMDGFCQYKQKWQVPIGTDFIREF				
Murine hepatitis pol 1ab (4395)		YCRSRVEHP-----DVDGLCKLRKRFVVGIGIKDPVSYV				
Consensus (4486)		YCRARVEHP-----DVDGLCQLKGKRFVQVPIGIGKDPVSEV				
Section 117						
	(4525)	4525	4530	4540	4550	4563
avian infectious bronchitis pol 1ab (3899)		LRNKVCTGQCWIGYGCQDGLRQPKSSVQSVAGASDFD				
bovine coronavirus pol 1ab (4343)		LTNDVCGVCGFWRDGSQVST-----TTVQSKD				
Human corona 229E pol 1ab (4044)		LENTCKVCGCLNHGCTDRT-----ATQSF				
Murine hepatitis pol 1ab (4430)		LTNDVCGVCGFWRDGSQVCTG-----SQVQSKD				
Consensus (4525)		LTNDVCQVCGFWRDGSQVST-----SAIQSKD				
Section 118						
	(4564)	4564	4570	4580	4590	4602
avian infectious bronchitis pol 1ab (3938)		KNYLNVRGSS-EARLIPLASCDPPDVVKATDVC KES				
bovine coronavirus pol 1ab (4373)		TNELNVRGTSVDRLVPCASGLSTIVOLAPDICNASV				
Human corona 229E pol 1ab (4072)		NSYLNVRGSS--SARLEPCNSTDIYCVAPDVY KDA				
Murine hepatitis pol 1ab (4460)		TNELNVRGTSVNARLVPCASGLDTPVOLAPDICANR				
Consensus (4564)		TNELNVRGSSVDARLVPCASGLDTPVOLRAFDICNKDA				
Section 119						
	(4603)	4603	4610	4620	4630	4641
avian infectious bronchitis pol 1ab (3976)		AGMFQNLKRNATPQEDDTEDGNLEYLSYFVVKQTPP				
bovine coronavirus pol 1ab (4412)		AGIGELNLVNCCTQQRVDENG-----KLDFFVVKRTDL				
Human corona 229E pol 1ab (4109)		SFVGKNDLSVPTKNVDKD-----AFYIARCIK				
Murine hepatitis pol 1ab (4499)		AGIGLYYIVNCPQQRVDEDG-----KLDFFVVKRTNL				
Consensus (4603)		AGIGLNLKVNCCRQQRVDEDGD-----KLDAFFVVKRTL				
Section 120						
	(4642)	4642	4650	4660	4670	4680
avian infectious bronchitis pol 1ab (4015)		SNYHEKSCYEDLSS-EVADHDIVENKN---LYNTS				
bovine coronavirus pol 1ab (4447)		TIYNFEMECYERVDCKFVAENDFTFDVEGSRVPNIV				
Human corona 229E pol 1ab (4140)		SVMDHOSMNLCCNVMKHDATWHEGRTIYGNVS				
Murine hepatitis pol 1ab (4534)		EVYNKSKCYELTDCGVVETEDFTFDVEGSRVPNIV				
Consensus (4642)		SVYNHEKSCYELLKDCVVAEHDFFTFDVEGSRVPNIVR				

**FIGURE 4A (contd.)**

Section 121				
	(4681)	4681	4690	4700
avian infectious bronchitis pol 1ab (4050)		QRNIRKYYTMMDFCYALRHFPKSC	EVVKETLV	TYGCCIEDY
bovine coronavirus pol 1ab (4486)		KDLTRYTALMLCYALRHFDNRDCE	MLCDIL	LSIYAGCEQS
Human corona 229E pol 1ab (4179)		QDLTRYTMMDLCEALRHFDNRDCE	MLKEIL	VLTGCCSTB
Murine hepatitis pol 1ab (4573)		KDLTRYTALMLCYALRHFDNRDCE	STLKEIL	LYAECEES
Consensus (4681)		QDLTKYTMLDLCYALRHFDNRDCE	EVVKETLV	TYACCEDS
Section 122				
	(4720)	4720	4730	4740
avian infectious bronchitis pol 1ab (4089)		HPKWFEEHNDWYDPIENSKYYV	MLARMG	ETVPRALLNAI
bovine coronavirus pol 1ab (4525)		Y----ETKFDWYDFVSNPDI	INVYKKG	PIFNRAIVSAT
Human corona 229E pol 1ab (4218)		Y----FEMKNGFLPTELEDTHRV	YAALSK	MANAMDKCM
Murine hepatitis pol 1ab (4612)		Y----EOKKDWYDFVSNPDI	INVYKKG	ETFNRAIVNTA
Consensus (4720)		Y	FEKKDWYDPIENPDI	INVYKKGPIVNRALLNAI
Section 123				
	(4759)	4759	4770	4780
avian infectious bronchitis pol 1ab (4128)		EEGNLMZEKSYVAVILLDNQD	LNGKFD	EGDEOKTAPGA
bovine coronavirus pol 1ab (4560)		EEADKIYEVLLYQRLSLDNQD	LNGKWD	EFQDYVIAAPGC
Human corona 229E pol 1ab (4253)		AHCDEMFLKCVFVLLDNQD	LNGNEIF	QDFVLCPPUM
Murine hepatitis pol 1ab (4647)		KEADAAEAGLYVLELDNQD	LYGOWY	DFGDEVKTVRGC
Consensus (4759)		EFAD	LVEKGLVGVLTLDNQDL	NGKFYDEGDFVKTAPGC
Section 124				
	(4798)	4798	4810	4820
avian infectious bronchitis pol 1ab (4167)		GVPVFEDTYSSYMMPLTTHALD	SEL	FN D
bovine coronavirus pol 1ab (4599)		GVATADSYSSYMMPLTTHALD	SEL	FN D
Human corona 229E pol 1ab (4292)		GVPYCTSYSSYMMPLTTHALD	SEL	FN D
Murine hepatitis pol 1ab (4686)		GVAVADSYSSYMMPLTTHALD	SEL	FN D
Consensus (4798)		GVPVADSYSSYMMPLTTHALD	SEL	FN D
Section 125				
	(4837)	4837	4850	4860
avian infectious bronchitis pol 1ab (4205)		FDLLQYDFTDHKLELENKYE	KHWSQD	YHPNTVDC
bovine coronavirus pol 1ab (4633)		FDLLQYDFTDHKLELENKYE	KHWSQD	YHPNTVDC
Human corona 229E pol 1ab (4331)		FDLLQYDFTDHKLELENKYE	KHWSQD	YHPNTVDC
Murine hepatitis pol 1ab (4720)		FDLLQYDFTDHKLELENKYE	KHWSQD	YHPNTVDC
Consensus (4837)		FDLLQYDFTDHKLELENKYE	KHWSQD	YHPNTVDC
Section 126				
	(4876)	4876	4890	4900
avian infectious bronchitis pol 1ab (4244)		IIHCANFNILFSTVIPTNTCE	GPLVRQ	IFVDGVPFVVSIG
bovine coronavirus pol 1ab (4672)		IIHCANFNILFSTVIPTNTCE	GPLVRQ	IFVDGVPFVVSIG
Human corona 229E pol 1ab (4370)		IIHCANFNILFSTVIPTNTCE	GPLVRQ	IFVDGVPFVVSIG
Murine hepatitis pol 1ab (4759)		IIHCANFNILFSTVIPTNTCE	GPLVRQ	IFVDGVPFVVSIG
Consensus (4876)		IIHCANFNILFSTVIPTNTCE	GPLVRQ	IFVDGVPFVVSIG

**FIGURE 4A (contd.)**

Section 127																																								
	(4915)	4915	4920	4930	4940	4953																																		
avian infectious bronchitis pol 1ab (4283)		YHS	AE	LG	VIM	QDNTMSFSKMGLSOLMOFVGERALLVGT																																		
bovine coronavirus pol 1ab (4711)		YHY	KE	LG	VIM	NMDVDTHRYRLSLKDLLLYAADI ALHVAS																																		
Human corona 229E pol 1ab (4409)		YHE	KO	TL	LV	WNKGVNTHSTRLTITELLQFVTDPTETIVAS																																		
Murine hepatitis pol 1ab (4798)		YHY	KE	LG	VIM	NMDVDTHRYRLSLKDLLLYAADI ALHVAS																																		
Consensus (4915)		YHY	KE	LG	VVM	NMDVDTHRYRLSLKDLLQFVADPALHVAS																																		
Section 128																																								
	(4954)	4954	4960	4970	4980	4992																																		
avian infectious bronchitis pol 1ab (4322)		S	NN	L	V	DDRRSLFESVCAITSLITHQTVRPGHENADLDFA																																		
bovine coronavirus pol 1ab (4750)		A	S	A	L	YDEREGCFSAITSGVKFQTVRPGNANODEFDFT																																		
Human corona 229E pol 1ab (4448)		S	P	A	L	VFKLVGSAITSTGLTSQTVRPGHENNELYDNL																																		
Murine hepatitis pol 1ab (4837)		A	S	A	L	VDDRRSLFESVCAITSGVKFQTVRPGNANODEFDFT																																		
Consensus (4954)		A	S	A	L	VDLRTCCFSVAAITSGVTFQTVKPGNFNQDFYDFI																																		
Section 129																																								
	(4993)	4993	5000	5010	5020	5031																																		
avian infectious bronchitis pol 1ab (4361)		E	K	A	R	M	L	K	E	L	S	I	P	K	I	N	M	P	Q	T	G	N	A	I	N	V	D	E	R	R	N	R	P	T						
bovine coronavirus pol 1ab (4789)		L	S	K	G	L	L	K	E	G	S	S	V	D	L	K	H	F	F	F	T	Q	D	G	N	A	A	I	T	D	Y	N	Y	K	Y	N	R	P	T	
Human corona 229E pol 1ab (4487)		R	S	Q	G	F	E	D	L	S	L	T	K	K	F	F	E	T	A	K	G	D	A	L	K	E	D	R	Y	R	N	P	T							
Murine hepatitis pol 1ab (4876)		L	S	K	G	L	L	K	E	G	S	S	V	D	L	K	H	F	F	F	T	Q	D	G	N	A	A	I	T	D	Y	N	Y	K	Y	N	R	P	T	
Consensus (4993)		L	S	K	G	L	L	K	E	G	S	S	V	D	L	K	H	F	F	F	T	Q	D	G	N	A	A	I	T	D	Y	N	Y	K	Y	N	R	P	T	
Section 130																																								
	(5032)	5032	5040	5050	5060	5070																																		
avian infectious bronchitis pol 1ab (4400)		M	F	L	L	I	C	O	L	L	E	F	C	L	E	Y	S	K	T	E	C	E	G	G	C	I	P	A	S	Q	V	V	M	N	L	D	K	S		
bovine coronavirus pol 1ab (4828)		M	V	D	I	K	O	L	L	E	F	V	L	E	V	V	K	Y	F	E	I	Y	E	G	G	C	I	P	A	S	Q	V	I	V	N	N	Y	D	K	S
Human corona 229E pol 1ab (4526)		M	L	L	I	G	A	R	V	A	Y	Q	A	A	R	E	D	C	E	G	C	I	L	T	S	R	E	V	M	T	H	L	N	K	S					
Murine hepatitis pol 1ab (4915)		M	V	D	I	K	O	L	L	E	F	V	L	E	V	V	K	Y	F	E	I	Y	E	G	G	C	I	P	A	S	Q	V	I	V	N	N	Y	D	K	S
Consensus (5032)		M	V	D	I	K	O	L	L	E	F	V	L	E	V	V	K	Y	F	E	I	Y	E	G	G	C	I	P	A	S	Q	V	I	V	N	N	Y	D	K	S
Section 131																																								
	(5071)	5071	5080	5090		5109																																		
avian infectious bronchitis pol 1ab (4439)		A	G	Y	P	N	K	F	G	K	A	R	L	Y	E	A	L	S	F	E	E	Q	D	E	I	F	A	Y	T	K	R	N	V	L	P	T	L	T		
bovine coronavirus pol 1ab (4867)		A	G	Y	P	N	K	F	G	K	A	R	L	Y	E	A	L	S	F	E	E	Q	D	E	I	F	A	Y	T	K	R	N	V	L	P	T	L	T		
Human corona 229E pol 1ab (4565)		A	G	W	E	L	N	K	K	F	G	A	G	L	Y	E	A	L	S	F	E	E	Q	D	E	I	F	A	Y	T	K	R	N	V	L	P	T	L	T	
Murine hepatitis pol 1ab (4954)		A	G	Y	P	N	K	F	G	K	A	R	L	Y	E	A	L	S	F	E	E	Q	D	E	I	F	A	Y	T	K	R	N	V	L	P	T	L	T		
Consensus (5071)		A	G	Y	P	N	K	F	G	K	A	R	L	Y	E	A	L	S	F	E	E	Q	D	E	I	F	A	Y	T	K	R	N	V	L	P	T	L	T		
Section 132																																								
	(5110)	5110	5120	5130		5148																																		
avian infectious bronchitis pol 1ab (4477)		Q	M	N	L	K	Y	A	I	S	A	K	N	R	A	R	T	V	A	G	V	S	I	L	S	T	M	T	G	R	Q	F	H	Q	K	C	L	K	S	I
bovine coronavirus pol 1ab (4906)		Q	M	N	L	K	Y	A	I	S	A	K	N	R	A	R	T	V	A	G	V	S	I	L	S	T	M	T	G	R	Q	F	H	Q	K	C	L	K	S	I
Human corona 229E pol 1ab (4604)		Q	M	N	L	K	Y	A	I	S	A	K	N	R	A	R	T	V	A	G	V	S	I	L	S	T	M	T	G	R	Q	F	H	Q	K	C	L	K	S	I
Murine hepatitis pol 1ab (4993)		Q	M	N	L	K	Y	A	I	S	A	K	N	R	A	R	T	V	A	G	V	S	I	L	S	T	M	T	G	R	Q	F	H	Q	K	C	L	K	S	I
Consensus (5110)		Q	M	N	L	K	Y	A	I	S	A	K	N	R	A	R	T	V	A	G	V	S	I	L	S	T	M	T	G	R	Q	F	H	Q	K	C	L	K	S	I



**FIGURE 4A (contd.)**

Section 133						
	(5149)	5149	5160	5170	5187	
avian infectious bronchitis pol 1ab (4516)		VNTRNASVNLGCTLEFYEGWDNMLRRLIQGSEDPLEMLND				
bovine coronavirus pol 1ab (4945)		AATRCMPVATIGCTTKFYGGNDMLRRLIKDYDNPVLARGWD				
Human corona 229E pol 1ab (4643)		VATINATVNLGCTIKFYGGWNNMLKNLMADVDDPKUMGWD				
Murine hepatitis pol 1ab (5032)		AATRCMPVATIGCTLEKTYGGNDMLRRLIKDYDSFVLMGWD				
Consensus (5149)		VATRNVPVVI GTTKFYGGWDNMLRRLIKDVDDPVLMGWD				
Section 134						
	(5188)	5188	5200	5210	5226	
avian infectious bronchitis pol 1ab (4555)		YPKCDRAMPNILRTAASSLVLARHTNCCSWSERIYRLYN				
bovine coronavirus pol 1ab (4984)		YPKCDRAMPNILRTIVSSSLVLARCHEACSSQSDRFYALAN				
Human corona 229E pol 1ab (4682)		YPKCDRAMPSMTMLMSAMTIGSKIVTECTASDKFYHLSQ				
Murine hepatitis pol 1ab (5071)		YPKCDRAMPNILRTIVSSSLVLARHTDSCSHEDREYALAN				
Consensus (5188)		YPKCDRAMPNILRTIVSSSLVLARKHDSCCS SDRFYRLAN				
Section 135						
	(5227)	5227	5240	5250	5265	
avian infectious bronchitis pol 1ab (4594)		ECAQVLSITLATGCIYVKPGGTSSGDATTAYANSVFNI				
bovine coronavirus pol 1ab (5023)		ECAQVLSITLMCGGCYVVKGTSSGDATTAFANSVFNI				
Human corona 229E pol 1ab (4721)		ELAQVITLEVYNSNGEYFRPGGTSSGDATTAYANSVFNI				
Murine hepatitis pol 1ab (5110)		ECAQVLSITLMCGGCYVVKPGGTSSGDATTAFANSVFNI				
Consensus (5227)		ECAQVLS EIVMCGGGYVVKPGGTSSGDATTAFANSVFNI				
Section 136						
	(5266)	5266	5280	5290	5304	
avian infectious bronchitis pol 1ab (4633)		IQATSANVARLLSVITRDIVYDNIKSLQYETVQOYVIRV				
bovine coronavirus pol 1ab (5062)		CQAVSANVCALMSCNGNKIEDLSIRALQKRRLYSIVYFSD				
Human corona 229E pol 1ab (4760)		FCQAVSNINCVLNVNSNCCNNENVKLCRQELDNCYENS				
Murine hepatitis pol 1ab (5149)		CQAVSANVCSLMACNGHKIEDLSIRALQKRRLYSNVYFAD				
Consensus (5266)		CQAVSANVCALLSVNG KIEDLSIKALQKRRLYSNVYRAD				
Section 137						
	(5305)	5305	5310	5320	5330	5343
avian infectious bronchitis pol 1ab (4672)		NVDPAFVSEKESYLCNNALMLSLDDGVVCYNNTLAKOG				
bovine coronavirus pol 1ab (5101)		MVISTATTEYEEFLNAHTSMMILSDDGVVCYNSDYASKG				
Human corona 229E pol 1ab (4799)		NVLESFVDDFGYIQKHFSMMILSITPSWGLNKTYGLG				
Murine hepatitis pol 1ab (5188)		NVDPAFVSEYEEFLNKHFSMMILSDDGVVCSEERASKG				
Consensus (5305)		NVDPAFVSEFYEEFLNKHFSMMILSDDGVVCYNSTYASKG				
Section 138						
	(5344)	5344	5350	5360	5370	5382
avian infectious bronchitis pol 1ab (4711)		LVADITGIREVLYYONNLYADSCQVYFPLEKGPHEFC				
bovine coronavirus pol 1ab (5140)		YIANISAFQOQVLYYONNVFMSESAKCVENDINNCPHEFC				
Human corona 229E pol 1ab (4838)		YIADISAFKATLYYONGVFMSTAKCTEEDLSIGVHEFC				
Murine hepatitis pol 1ab (5227)		YIANISAFQOQVLYYONNVFMSESAKCVETDIEKGPHEFC				
Consensus (5344)		YIANISAFQOQVLYYONNVFMSEAKCWVE DIEKGPHEFC				

**FIGURE 4A (contd.)**

Section 139					
	(5383)	5383	5390	5400	5410 5421
avian infectious bronchitis pol 1ab (4750)		SCHTMLV	VDGEPKYL	YPDPSR	HLGACMPYVDVDRLEP
bovine coronavirus pol 1ab (5179)		SCHTMLVKMDGDDVYL	YPDPSR	HLGAGCFVDDLLKTD	
Human corona 229E pol 1ab (4877)		SCHTMQIVDENGKYL	YPDPSR	HLGAGVFVDDLLKTD	
Murine hepatitis pol 1ab (5266)		SCHTMLVKMDGDDVYL	YPDPSR	HLGAGCFVDDLLKTD	
Consensus (5383)		SQHTMLVKMDGDDVYL	YPDPSR	HLGAGVFVDDLLKTD	
Section 140					
	(5422)	5422	5430	5440	5450 5460
avian infectious bronchitis pol 1ab (4789)		VAVMEAYTALA	AYPLVH	ENEERYKVF	FMLLAYTRKE
bovine coronavirus pol 1ab (5218)		VLLIERFVSLA	DAYPLV	YHENEERYQK	VERVMLEYIKKE
Human corona 229E pol 1ab (4916)		VLLIERFVSLA	DAYPL	SKHPN	PERKAYALLDVKHH
Murine hepatitis pol 1ab (5305)		VLLIERFVSLA	DAYELV	YHENEERYQK	VERVMLEYIKKE
Consensus (5422)		VLLIERFVSLA	DAYPLV	YHENEERYQK	VERVMLEYIKKE
Section 141					
	(5461)	5461	5470	5480	5490
avian infectious bronchitis pol 1ab (4828)		YNDLGNQIL	DSYSVIL	STCDGSK	FWEDESYKNMYLRSTV
bovine coronavirus pol 1ab (5257)		YNDLGNQIL	DSYSVIL	STCDGSK	FWEDESYKNMYLRSTV
Human corona 229E pol 1ab (4955)		NKTIN	EGVLESE	VTILDEHES	KWDESYKASMEKSTV
Murine hepatitis pol 1ab (5344)		YNDLGNQIL	DSYSVIL	STCDGSK	FWEDESYKNMYLRSTV
Consensus (5461)		YNDLGNQIL	DSYSVIL	STCDGSK	FWEDESYKNMYLRSTV
Section 142					
	(5500)	5500	5510	5520	5530
avian infectious bronchitis pol 1ab (4867)		LQSCGVV	CNSQTS	LRGSCIRK	PLLCCKCCYDHVMAT
bovine coronavirus pol 1ab (5296)		LQSVGAC	VVCSQTS	LRGSCIRK	PLLCCKCCYDHVMAT
Human corona 229E pol 1ab (4994)		LQAGL	QVCGSV	VRCDCLDR	FMCTMCAIDHVEGT
Murine hepatitis pol 1ab (5383)		LQSVGAC	VVCSQTS	LRGSCIRK	PLLCCKCCYDHVMAT
Consensus (5500)		LQSVGAC	VVCSQTS	LRGSCIRK	PLLCCKCCYDHVMAT
Section 143					
	(5539)	5539	5550	5560	5570
avian infectious bronchitis pol 1ab (4906)		DLKNVLS	ISPNPT	CSQLGGCEAD	YVGLTSGMSYYCEDHK
bovine coronavirus pol 1ab (5335)		CHKYVLS	ISPNPT	CSQLGGCEAD	YVGLTSGMSYYCEDHK
Human corona 229E pol 1ab (5033)		DLKNVLS	ISPNPT	CSQLGGCEAD	YVGLTSGMSYYCEDHK
Murine hepatitis pol 1ab (5422)		CHKYVLS	ISPNPT	CSQLGGCEAD	YVGLTSGMSYYCEDHK
Consensus (5539)		CHKYVLS	ISPNPT	CSQLGGCEAD	YVGLTSGMSYYCEDHK
Section 144					
	(5578)	5578	5590	5600	5610
avian infectious bronchitis pol 1ab (4945)		PNLSIP	PLVSNQ	TYRANG	AGSENVDDFNOLATTVS
bovine coronavirus pol 1ab (5374)		PQYSF	PLVSNQ	TYRANG	AGSENVDDFNOLATTVS
Human corona 229E pol 1ab (5072)		PNLSIP	PLVSNQ	TYRANG	AGSENVDDFNOLATTVS
Murine hepatitis pol 1ab (5461)		PQYSF	PLVSNQ	TYRANG	AGSENVDDFNOLATTVS
Consensus (5578)		PQYSF	PLVSNQ	TYRANG	AGSENVDDFNOLATTVS

**FIGURE 4A (contd.)**

Section 145					
	(5617) 5617	5630	5640	5655	
avian infectious bronchitis pol 1ab (4984)	IVEPPTLEANRCSDSERRFAAEVVKATDELHQDPASAEV				
bovine coronavirus pol 1ab (5413)	DVDDYILANECTERLKLFAAEVQKATDAEKQSYASATI				
Human corona 229E pol 1ab (5111)	DTTDYKLANDAKESRLFAAEVVKAKESVVSSTAYATE				
Murine hepatitis pol 1ab (5500)	EVDDYVLANECTERLKLFAAEVQKATEEAFKQCYASATI				
Consensus (5617)	DVDDYILANECTESLKLFAAEVVKATEEAFKQSYASATI				
Section 146					
	(5656) 5656	5670	5680	5694	
avian infectious bronchitis pol 1ab (5023)	REIVSDRELILSWEIPGTRDELNRUYVETGYHFTKNSKV				
bovine coronavirus pol 1ab (5452)	QELVSERELILSWEIGVKPPLNKNYVETGYHFTKNSKT				
Human corona 229E pol 1ab (5150)	REIVGPKLLILLWESGNAKFFLNRSVETCEQIKDSKF				
Murine hepatitis pol 1ab (5539)	REIVSDRELILSWEIGVKPPLNKNYVETGYHFTKNSKT				
Consensus (5656)	REIVSDRELILSWEIGVKPPLNKNYVETGYHFTKNSKT				
Section 147					
	(5695) 5695	5700	5710	5720	5733
avian infectious bronchitis pol 1ab (5062)	QLQDETLEEGEGKDV-VYKATSAKTSVDTVITSHN				
bovine coronavirus pol 1ab (5491)	VLGEYVEDNSELTNG-VYRATTTYKLSVDVDTSHS				
Human corona 229E pol 1ab (5189)	QMGREVEVDYGGDTMTKSLATTKLVPMLALLSHN				
Murine hepatitis pol 1ab (5578)	VLGEYVEDNSELTNG-VYRATTTYKLSVDVDTSHS				
Consensus (5695)	VLGEYVEDNSELTNG-VYKATTTYKLSVGDVFIITSHN				
Section 148					
	(5734) 5734	5740	5750	5760	5772
avian infectious bronchitis pol 1ab (5100)	VVSDVARBCPQOTFSRFVNRNVNVPCECVNTEPLYH				
bovine coronavirus pol 1ab (5529)	VANISAPTLVPQE-NYSSIRFASVYSVLETQNNVNYQ				
Human corona 229E pol 1ab (5228)	VAPIRPMANCKYSTIYKEHPSENVSDANLVPIYO				
Murine hepatitis pol 1ab (5616)	VSSISAPTLVPQE-NYTSIRFASVYSVPETFOQNVNYQ				
Consensus (5734)	VASLSAPTLVPQE NYTSIRLASVYSVPETFOQNVNYQ				
Section 149					
	(5773) 5773	5780	5790	5800	5811
avian infectious bronchitis pol 1ab (5139)	LVGKQRRTLVGGPFGSGKSHFAIGLAVVYCTARVVFTAC				
bovine coronavirus pol 1ab (5567)	HIGMRYCTVQGPFGSGKSHLAIGLAVVYCTARVVFTAA				
Human corona 229E pol 1ab (5267)	LIGKQRITLVGGPFGSGKSHFAIGLAVVYCTARVVFTAC				
Murine hepatitis pol 1ab (5654)	HIGMRYCTVQGPFGSGKSHFAIGLAVVYCTARVVFTAA				
Consensus (5773)	LIGMQRYYTTVQGPFGSGKSHLAIGLAVVYCTARVVFTAC				
Section 150					
	(5812) 5812	5820	5830	5840	5850
avian infectious bronchitis pol 1ab (5178)	SHAAVDALCEKAHKFELNINDCTRIVPAKVRVDCYSKEKA				
bovine coronavirus pol 1ab (5606)	SHAAVDALCEKAHKFELNINDCTRIVPAKVRVDCYSKEKI				
Human corona 229E pol 1ab (5306)	SHAAVSTCAAVTAYSVDKCTETIFARARECYSGEKFP				
Murine hepatitis pol 1ab (5693)	SHAAVDALCEKAHKFELNINDCTRIVPAKVRVDCYSKEKV				
Consensus (5812)	SHAAVDALCEKAHKFELNINDCTRIVPAKVRVDCYSKEKI				

**FIGURE 4A (contd.)**

Section 151					
	(5851)	5851	5860	5870	5889
avian infectious bronchitis pol 1ab (5217)	NDT	GKKYIFST	TINALPEVSC	ITLVDVSM	LTNYELSVI
bovine coronavirus pol 1ab (5645)	NDT	TRKYVET	TINALPEMVT	QIVVVEV	SMLENYELSVI
Human corona 229E pol 1ab (5345)	NNH	SQYVST	TNALPEVNAD	IVVVEV	SMCNYELSVI
Murine hepatitis pol 1ab (5732)	NDT	TRKYVET	TINALPELVTD	QIVVVEV	SMLENYELSVI
Consensus (5851)	NDT	TRKYVET	TINALPEVVT	DIVVVEV	SMLENYELSVI
Section 152					
	(5890)	5890	5900	5910	5928
avian infectious bronchitis pol 1ab (5256)	NCK	INYYV	VQDPAQLP	APRVL	LLSG-KDYL
bovine coronavirus pol 1ab (5684)	NAR	IRAKHY	YIGDPAQLP	AEVLL	SKGTLEPKY
Human corona 229E pol 1ab (5384)	NCR	ISYKH	IIVVCD	FQYPA	LVTSKGVMEIDY
Murine hepatitis pol 1ab (5771)	NSR	VSARKY	YIGDPAQLP	AEVLL	SKGTLEPKY
Consensus (5890)	NAR	ISYKH	YIGDPAQLP	APRVLL	SKGTLEPKY
Section 153					
	(5929)	5929	5940	5950	5967
avian infectious bronchitis pol 1ab (5294)	NLM	VCVK	ILFLAK	YRCK	KETD
bovine coronavirus pol 1ab (5723)	KL	CCLG	PDIL	GT	CPKEIV
Human corona 229E pol 1ab (5423)	QR	CAIG	UDV	FLHK	CPDALT
Murine hepatitis pol 1ab (5810)	KL	CCLG	PDIL	GT	CPKEIV
Consensus (5929)	KLM	CCLG	PDIL	GT	CPKEIV
Section 154					
	(5968)	5968	5980	5990	6006
avian infectious bronchitis pol 1ab (5333)	PEE	RECE	AVIVN	NGNSD	MGHES
bovine coronavirus pol 1ab (5762)	ES	SL	PRV	YKGG	---
Human corona 229E pol 1ab (5462)	EA	KQ	TF	FERG	---
Murine hepatitis pol 1ab (5849)	DN	ES	MO	KVYK	---
Consensus (5968)	EAS	SL	CFK	VYKGG	---
Section 155					
	(6007)	6007	6020	6030	6045
avian infectious bronchitis pol 1ab (5372)	RN	KQ	RE	AI	FE
bovine coronavirus pol 1ab (5798)	AN	PL	HK	VE	ES
Human corona 229E pol 1ab (5498)	KN	ST	SK	AV	FE
Murine hepatitis pol 1ab (5885)	AN	PS	SK	AV	FE
Consensus (6007)	AN	PS	SK	AV	FE
Section 156					
	(6046)	6046	6060	6070	6084
avian infectious bronchitis pol 1ab (5411)	YDY	V	IESQ	AETA	SV
bovine coronavirus pol 1ab (5837)	YDY	V	IESQ	AETA	SV
Human corona 229E pol 1ab (5537)	YDY	V	IESQ	AETA	SV
Murine hepatitis pol 1ab (5924)	YDY	V	IESQ	AETA	SV
Consensus (6046)	YDY	V	IESQ	AETA	SV

**FIGURE 4A (contd.)**

Section 157						
	(6085)	6085	6090	6100	6110	6123
avian infectious bronchitis pol 1ab (5450)		DELYSALKFT	ELDSETS	-----	LQGTGLEN	IGNKEES
bovine coronavirus pol 1ab (5876)		QLFEALQFT	TLTLDDKVP	QAVETR	VQCSTN	LKDCSKSYS
Human corona 229E pol 1ab (5576)		TLEDAK	HFETIMTDLQ	-----	SESS	CGLEKDEARNPI
Murine hepatitis pol 1ab (5963)		QLFESLN	FTTLTLDKIN	---	NPRLOCTN	PKDCSRSYV
Consensus (6085)		QLFEALN	FTTLTLDKIN		RLQCSTN	LKDCSKSYS
Section 158						
	(6124)	6124	6130	6140	6150	6162
avian infectious bronchitis pol 1ab (5482)		GVHAYAV	TTKALAAT	YKVNDEL	AALVN	VEAGSETTKN
bovine coronavirus pol 1ab (5915)		GYHPAH	PSFLAVDD	KYKATGD	LAVCL	IGDS-AVTSR
Human corona 229E pol 1ab (5609)		DLPD	SHATYLS	SDREKT	SGDL	VOICNNN--VCNTEH
Murine hepatitis pol 1ab (5999)		GYHPAH	PSFLAVDD	KYKVGGL	AVCLNV	ADS-AVTSR
Consensus (6124)		GYHPAH	APSFLALDD	KYKVSGL	AVCLNV	ADS AVTYSR
Section 159						
	(6163)	6163	6170	6180	6190	6201
avian infectious bronchitis pol 1ab (5521)		LISLM	GKMSVN	VECHNM	ITRDE	IKRVRAVGFEDV
bovine coronavirus pol 1ab (5953)		LISLM	GKLDVTL	DYCKLE	ITKEE	AVRRAVGFEDV
Human corona 229E pol 1ab (5646)		MTYMG	IRFDVSM	PCSHGL	CIRDF	MRHRAVGLMEVE
Murine hepatitis pol 1ab (6037)		LISLM	GKLDLTL	DYCKLE	ITRDE	IKRVRAVGFEDV
Consensus (6163)		LISLM	GFKLDVTL	DGYHKL	FITRDE	AIKRVRAVWGFEDVE
Section 160						
	(6202)	6202	6210	6220	6230	6240
avian infectious bronchitis pol 1ab (5560)		ATHACGT	NFTLPLP	SVSPAT	CADEV	VTPPELVDSIGN
bovine coronavirus pol 1ab (5992)		GAHATRD	STGTNFTL	QLGSTG	EDTVEAT	CFADRGGY
Human corona 229E pol 1ab (5685)		GAIVT	GDVGLV	LVGV	FNQVD	VAQPECCVLNTGS
Murine hepatitis pol 1ab (6076)		GAHATRD	STGTNFTL	QLGSTG	EDTVEAT	MFAERDGY
Consensus (6202)		GAHATRD	SIGTNFP	PLQLGF	STGIDF	VVEPTGLVATRDGY
Section 161						
	(6241)	6241	6250	6260		6279
avian infectious bronchitis pol 1ab (5599)		NEEPVN	SKAPGGE	QNNHER	VFKSA	KPWHTTPTVQML
bovine coronavirus pol 1ab (6031)		SEKKAV	AKKPPGE	QKHLIP	LMTRG	QRDVPVRIVQML
Human corona 229E pol 1ab (5724)		VVKEV	RARPLGL	QTHIVP	LRKGQ	PSVLLKRVQML
Murine hepatitis pol 1ab (6115)		VEKKAA	ARAPGGE	QKHLIP	PLMSR	GQKPDVVRIVQML
Consensus (6241)		VFKPV	AKAPPGE	QPKHLI	PLMSR	GQPDVVRIVQML
Section 162						
	(6280)	6280	6290	6300		6318
avian infectious bronchitis pol 1ab (5638)		ADHL	CNVSD	CVVPM	TCHGL	TLTPVITC-KEQVCS
bovine coronavirus pol 1ab (6070)		ADHL	IDLSD	CVLT	TWAAN	FELCLLNAVCRRTSGNV
Human corona 229E pol 1ab (5763)		ADFL	ACSSV	LEFL	LAGCE	DTTMTPTVITC-AVKHCO
Murine hepatitis pol 1ab (6154)		SDH	ADLAD	SVLT	TWAAS	FELCLLNAVCRREVVCNV
Consensus (6280)		ADHL	ADLSD	CVVLT	TWAAG	LELTTLRYFVKIGREV CCV

**FIGURE 4A (contd.)**

Section 163																			
	(6319)	6319	6330	6340	6357														
avian infectious bronchitis pol 1ab (5676)		EGSRARTEN	SHHQAA	ACWKHC	LGFDVYN	DLVDLQ	QW												
bovine coronavirus pol 1ab (6109)		CTKRATAY	NCRTGY	YGWRH	SVTC	DYLY	PLIVDI	QQW											
Human corona 229E pol 1ab (5801)		CGTV	TCYNE	VSND	CGPKHALG	CDYV	NYMID	QQW											
Murine hepatitis pol 1ab (6193)		CTKRATC	EN	RTGY	YGWRH	SYSG	UYLYN	PLIVDI	QQW										
Consensus (6319)		CTKRATCF	NSRTGY	YGCKH	SLG	CDYLYN	PLIVDI	QQW											
Section 164																			
	(6358)	6358	6370	6380	6396														
avian infectious bronchitis pol 1ab (5715)		YSGN	ICFES	DLHON	VHGH	AVASV	CAIM	TRCL	AINNAFC										
bovine coronavirus pol 1ab (6148)		YIGS	ISSH	DLYL	SVHKG	AHVASS	DAIM	TRCL	AVYDCFC										
Human corona 229E pol 1ab (5840)		YVGS	ISTH	HAIC	NVRNE	IVAS	GDAM	TRCL	AVYDCFC										
Murine hepatitis pol 1ab (6232)		YIGS	ITSN	HDPL	SVHKG	AHVASS	DAIM	TRCL	AVYDCFC										
Consensus (6358)		YTGSL	SSNHD	LICS	SVHKG	AHVASS	DAIM	TRCL	AVYDCFC										
Section 165																			
	(6397)	6397	6410	6420	6435														
avian infectious bronchitis pol 1ab (5754)		QDVN	DLTY	PHIA	DEV	SSCH	YL	ORMY	LNAC	VDALKV									
bovine coronavirus pol 1ab (6187)		NNIN	NVE	PLI	SL	LSI	TP	SC	VL	RVMLK	AMLCNRY								
Human corona 229E pol 1ab (5879)		KNVD	SITY	PIA	HN	AI	KG	GT	TV	SHIM	RAIKLYNP								
Murine hepatitis pol 1ab (6271)		KSVN	NLE	PII	LS	TV	SV	TP	SC	VL	RVMLK	AMLCNRY							
Consensus (6397)		KNVN	WNLT	YPII	ANELS	INT	SC	RL	LQ	RVML	RAAMLCNRY								
Section 166																			
	(6436)	6436	6450	6460	6474														
avian infectious bronchitis pol 1ab (5793)		NVYV	DLN	PKGI	KCV	RRGD	VNER	KN	IVR	NV	QFE								
bovine coronavirus pol 1ab (6226)		TLCY	D	PKGI	---	AIAC	VK	DF	EF	KFYD	KN	PIVKS	SV	TLL					
Human corona 229E pol 1ab (5918)		KAIH	D	PKGI	---	GIR	CA	VD	DA	WYC	KN	INS	NV	TLE					
Murine hepatitis pol 1ab (6310)		DVYV	DLN	PKGI	---	GLAC	VK	DF	EF	KFYD	KN	PIVKS	SV	QFV					
Consensus (6436)		VCYD	IGN	PK	---	AIAC	VK	DF	EF	KFYD	KN	PIVKS	SV	KTLE					
Section 167																			
	(6475)	6475	6480	6490	6500	6513													
avian infectious bronchitis pol 1ab (5831)		YDYN	Q	KD	KEAD	SL	CM	FW	N	CV	DN	SL	DR	Y	TRNL				
bovine coronavirus pol 1ab (6262)		Y	EEA	KD	SEK	SL	CM	FW	N	CV	DN	SL	DR	Y	TRNL				
Human corona 229E pol 1ab (5955)		YDYM	T	G	---	QM	GL	CL	FW	N	CV	DN	SL	DR	Y	TRNL			
Murine hepatitis pol 1ab (6346)		YKYEA	KD	QFL	SL	CM	FW	N	CV	DN	SL	DR	Y	TRNL					
Consensus (6475)		YDYE	AHKD	FL	DGL	CM	FW	N	CV	DN	SL	DR	Y	TRNL					
Section 168																			
	(6514)	6514	6520	6530	6540	6552													
avian infectious bronchitis pol 1ab (5870)		SVEN	LP	CG	CG	SLY	VN	KH	AF	HT	PP	FD	RA	AF	EN	LK	PM	PEF	
bovine coronavirus pol 1ab (6301)		NNL	LP	CG	CG	SLY	VN	KH	AF	HT	PP	FD	RA	AF	EN	LK	PM	PEF	
Human corona 229E pol 1ab (5992)		STL	LP	CG	CG	SLY	VN	KH	AF	HT	PP	FD	RA	AF	EN	LK	PM	PEF	
Murine hepatitis pol 1ab (6385)		NKL	LP	CG	CG	SLY	VN	KH	AF	HT	PP	FD	RA	AF	EN	LK	PM	PEF	
Consensus (6514)		S	LN	LP	GC	NG	SLY	VN	KH	AF	HT	PP	FD	RA	AF	EN	LK	PM	PEF

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**FIGURE 4A (contd.)**

Section 169					
	(6553)	6553	6560	6570	6580 6591
avian infectious bronchitis pol 1ab (5909)		FEDSSPGETLQVDCVAG-DLVSLATKDCITKCNIGGAVC			
bovine coronavirus pol 1ab (6340)		YYS DTPGVYMDGMDAKQVDYVPLRSATCITKCNIGGAVC			
Human corona 229E pol 1ab (6031)		YDDGSGCEVVDQVN----YVPLRAITNCTKCNIGGAVC			
Murine hepatitis pol 1ab (6424)		YYS DTPGVYMEGMECKQVDYVPLRSATCITKCNIGGAVC			
Consensus (6553)		YYS DTPGVYMDGMDAKQVDYVPLRSATCITKCNIGGAVC			
Section 170					
	(6592)	6592	6600	6610	6620 6630
avian infectious bronchitis pol 1ab (5947)		KKHAQMTAEFVTSNAAVTAGHTFVTKNLNPNYLLKSE			
bovine coronavirus pol 1ab (6379)		LKHAEEYREYLESYNTATTAGETFWVYKTFDFYNLWNTF			
Human corona 229E pol 1ab (6066)		SKHANLYRAYMEETNIFLQAGFNIVPTTEDCYNLLQTF			
Murine hepatitis pol 1ab (6463)		KKHAEEYREYLESYNTATTAGETFWVYKTFDFYNLWNTF			
Consensus (6592)		LKHAEEYREYLESYNTATTAGETFWVYKTFDFYNLWNTF			
Section 171					
	(6631)	6631	6640	6650	6669
avian infectious bronchitis pol 1ab (5986)		SAL--QSIDTAYNMYKGLHYDAIAEMITVITGDAFV			
bovine coronavirus pol 1ab (6418)		TKL--QSLENVYVNLVKTCHYTGOAGEMCALINDKVA			
Human corona 229E pol 1ab (6105)		TEVNLGLENIAFVVKSEVGDGELLVATSGDAFV			
Murine hepatitis pol 1ab (6502)		TRL--QSLENVYVNLVNAHGHDGRAGELCAVIGENVA			
Consensus (6631)		TKL QSLENIVYNLVNAGHFDG AGELPCAIIIGDKVFV			
Section 172					
	(6670)	6670	6680	6690	6708
avian infectious bronchitis pol 1ab (6023)		IDQGVKAVFVNQTTERTSVAFELYKKNIRTLENNRIE			
bovine coronavirus pol 1ab (6455)		KIQKEDVVIINNITYFINVAVLEFAKRSIRHHPELKEF			
Human corona 229E pol 1ab (6144)		RDGNTDNLVVFVETSEPTNIAFLEFAKRVGLTPLESTF			
Murine hepatitis pol 1ab (6539)		KIQNEDVVVFKNTPFENVAVLEFAKRSIRPHPELKEF			
Consensus (6670)		KIQNEDVVVFVNNTTLPNTVAVELFAKRSIR HPELKEF			
Section 173					
	(6709)	6709	6720	6730	6747
avian infectious bronchitis pol 1ab (6062)		KGIGMDVTNGFVTDYANQTEBYRNIVKVAAT--DIEP			
bovine coronavirus pol 1ab (6494)		RNINIDVCWKHINDYARESIFGSNVYGCMTDKEFID			
Human corona 229E pol 1ab (6183)		KNICMVATYKFLDQVEAERPLTSFKSVGYT--DEAE			
Murine hepatitis pol 1ab (6578)		RNINIDVCWKHINDYAKDSVFGSNVYKCKYTDLOCTE			
Consensus (6709)		KNLNIDVTWKHVIWDYAKESPLCSNTYKVCAYTDLDFIE			
Section 174					
	(6748)	6748	6760	6770	6786
avian infectious bronchitis pol 1ab (6099)		NGLVLYDDRYDYQSELAADNAFLVSTQCYKRYSYMEI			
bovine coronavirus pol 1ab (6533)		KENVLEDGRDNALAEAKRSNNGVYISTTKVSLSMIKG			
Human corona 229E pol 1ab (6220)		DVCTCYDYSIQSYERETLSTALASATAVTGCKS--			
Murine hepatitis pol 1ab (6617)		SENVLEDGRDNALAEAKKCRNGVYINTTKVSLSMIKG			
Consensus (6748)		LNVLFDGRDNGAYEAFKKS NAVYISTTKVKSLSMIKG			

**FIGURE 4A (contd.)**

Section 175					
	(6787) 6787	6800	6810	6825	
avian infectious bronchitis pol 1ab (6138)	PSNLLVQNGMPLKDGAN	-----	-----	LYVYKRVN-	
bovine coronavirus pol 1ab (6572)	PPRAELNGVVVDKVGDTDCVFEYFAVRKEGQDVIFSO FDS				
Human corona 229E pol 1ab (6257)	LPAIKLNFGLMNGNAIATVKSEDCNIKNINWFVYVEKDG				
Murine hepatitis pol 1ab (6656)	PQRADLNGVVVEKVGDSDVVEEFPAVRKDGDDVIFSPITGS				
Consensus (6787)	PPRADLNGVMVDKVGDSDV FWFVRKDGNDVIFSR DS				
Section 176					
	(6826) 6826	6840	6850	6864	
avian infectious bronchitis pol 1ab (6163)	-----	-----	GAFVTLPTNTINAGRSY		
bovine coronavirus pol 1ab (6611)	LRVSSNQSPQGNLGSNEPCNVGGNDALATSTIFTGSRVIT				
Human corona 229E pol 1ab (6296)	KPVDFHYDG	-----	-----	FMKIGRNL	
Murine hepatitis pol 1ab (6695)	LEPSSHYSPOGNPGGNRVGDESNEALARGTIFTCSILL				
Consensus (6826)	L VSHY SPQGN G N G L GNDALA TIFTQSRLL				
Section 177					
	(6865) 6865	6870	6880	6890	6903
avian infectious bronchitis pol 1ab (6180)	ETTEPRSDIPRDLAMSEESVERIG-KALGLQITLGE				
bovine coronavirus pol 1ab (6650)	SSFTCTDMKDNIALDDDLFIQKLGEEYAFEFIVYGN				
Human corona 229E pol 1ab (6312)	QDLEPSTMLELNNMDIGVFIQKYGLFENEEVYVGD				
Murine hepatitis pol 1ab (6734)	SSFTPRSEMHKMDLDDDDVFIKYSLODYAFEFVYGS				
Consensus (6865)	SSFTPRSDMEKDFLALDDDDVFIQKYGLDYAFEFHIVYGD				
Section 178					
	(6904) 6904	6910	6920	6930	6942
avian infectious bronchitis pol 1ab (6218)	VDKPOLGGTATVIGMYLLRANKETNAKSVTNSDSCVMQN				
bovine coronavirus pol 1ab (6689)	FNQKIIGGLHLLIGLYRRQTSNLVIQEFVSYDSSIHSY				
Human corona 229E pol 1ab (6351)	VSKITLGLLHLLSQVFLSKMCIKAEFEVAASDITLKC				
Murine hepatitis pol 1ab (6773)	FNQKIIGGLHLLIGLYRRQTSNLVIQEFVSYDSSIHSY				
Consensus (6904)	VNQKIIGGLHLLIGLYRRQQ SNLVIQEFVSYDSSIHSY				
Section 179					
	(6943) 6943	6950	6960	6970	6981
avian infectious bronchitis pol 1ab (6257)	YFVLSDNG-SYRQVCTVVDLLDDDFELLRLLKEYGTN				
bovine coronavirus pol 1ab (6728)	ELTDEKSG-GSKSVCTVIDLLDDFVALVKSLNLCVS-				
Human corona 229E pol 1ab (6390)	CTVTYLNDFSSKLVCTYMLLIDLRVSVLKSIDETVVS-				
Murine hepatitis pol 1ab (6812)	ELTDENSG-SSSVCTVIDLLDDFVDIVKSLNLCVS-				
Consensus (6943)	FIVDE SG SSKSVCTVIDLLDDFVELLKSINL CVS				
Section 180					
	(6982) 6982	6990	7000	7010	7020
avian infectious bronchitis pol 1ab (6295)	KSNVVTASIDYHGSINEMTWFEDGSIKCTPOTQS--AWT				
bovine coronavirus pol 1ab (6765)	--KVVNVNIDFKDFQFMLWCNDEKVMTFYPRQAASDWK				
Human corona 229E pol 1ab (6428)	--KYHEVITNKPWRWMLWCKDNAAVAFETQIGS-AENK				
Murine hepatitis pol 1ab (6849)	--KVVNVNIDFKDFQFMLWCNDEKVMTFYPRQAASDWK				
Consensus (6982)	KVVNVNIDFKDFQFMLWCNDEKVMTFYPRQAASDWK				



**FIGURE 4A (contd.)**

Section 181					
	(7021)	7021	7030	7040	7059
avian infectious bronchitis pol 1ab (6332)		CGNNMP	ELTKVQNCVM	PCNIP	MTAVGELLPSGITLMNVA
bovine coronavirus pol 1ab (6802)		PGTSM	PVLYKYLNSPMERVS	SLWNYCKEVTLET	SCMMNVA
Human corona 229E pol 1ab (6464)		CGTSM	GLYNTORMCLEPCNLYN	YGAGLKLPSGIMFN	NAV
Murine hepatitis pol 1ab (6886)		PGYVM	PVLYKYLESPLE	RVNLWNYGKPI	TLTGSCMMNVA
Consensus (7021)		PGYSMP	VLYKYQNSPLERVNLWNYGKPI	TLPSGIMM	NVA
Section 182					
	(7060)	7060	7070	7080	7098
avian infectious bronchitis pol 1ab (6371)		KYTQLCQYLST	TTLCVPHNMRV	LHLGAGSDKGVAPGSAV	
bovine coronavirus pol 1ab (6841)		KYTQLCQYLST	TTLCVPHNMRV	LHLGAGSDKGVAPGSAV	
Human corona 229E pol 1ab (6503)		KYTQLCQYLST	TTLCVPHNMRV	LHLGAGSDKGVAPGSAV	
Murine hepatitis pol 1ab (6925)		KYTQLCQYLST	TTLCVPHNMRV	LHLGAGSDKGVAPGSAV	
Consensus (7060)		KYTQLCQYLST	TTLCVPHNMRV	LHLGAGSDKGVAPGSAV	
Section 183					
	(7099)	7099	7110	7120	7137
avian infectious bronchitis pol 1ab (6410)		LKQWLPAGTIL	VDNDVVPFVS	DAVASYFGDCITLPFDCQ	
bovine coronavirus pol 1ab (6880)		LKQWLPAGTIL	VDNDVVPFVS	DAVASYFGDCITLPFDCQ	
Human corona 229E pol 1ab (6542)		LKQWLPAGTIL	VDNDVVPFVS	DAVASYFGDCITLPFDCQ	
Murine hepatitis pol 1ab (6964)		LKQWLPAGTIL	VDNDVVPFVS	DAVASYFGDCITLPFDCQ	
Consensus (7099)		LKQWLPAGTIL	VDNDVVPFVS	DAVASYFGDCITLPFDCQ	
Section 184					
	(7138)	7138	7150	7160	7176
avian infectious bronchitis pol 1ab (6449)		FDLIISDMYD	PITKNIGEYNVSK	----	DGFFTYICHMIR
bovine coronavirus pol 1ab (6919)		FDLIISDMYD	PITKNIGEYNVSK	----	DGFFTYICHMIR
Human corona 229E pol 1ab (6581)		FDLIISDMYD	PITKNIGEYNVSK	----	DGFFTYICHMIR
Murine hepatitis pol 1ab (7003)		FDLIISDMYD	PITKNIGEYNVSK	----	DGFFTYICHMIR
Consensus (7138)		FDLIISDMYD	PITKNIGEYNVSK	----	DGFFTYICHMIR
Section 185					
	(7177)	7177	7190	7200	7215
avian infectious bronchitis pol 1ab (6488)		NNIALGGSVAIK	ITEFSWNAELY	DLMOKFAFWTMECTNV	
bovine coronavirus pol 1ab (6954)		NNIALGGSVAIK	ITEFSWNAELY	DLMOKFAFWTMECTNV	
Human corona 229E pol 1ab (6616)		NNIALGGSVAIK	ITEFSWNAELY	DLMOKFAFWTMECTNV	
Murine hepatitis pol 1ab (7038)		NNIALGGSVAIK	ITEFSWNAELY	DLMOKFAFWTMECTNV	
Consensus (7177)		NNIALGGSVAIK	ITEFSWNAELY	DLMOKFAFWTMECTNV	
Section 186					
	(7216)	7216	7230	7240	7254
avian infectious bronchitis pol 1ab (6527)		NASSEAF	LIGINYLG	----	KPKVEIDNVMHANYLFWRNS
bovine coronavirus pol 1ab (6993)		NASSEAF	LIGINYLG	----	KPKVEIDNVMHANYLFWRNS
Human corona 229E pol 1ab (6655)		NASSEAF	LIGINYLG	----	KPKVEIDNVMHANYLFWRNS
Murine hepatitis pol 1ab (7077)		NASSEAF	LIGINYLG	----	KPKVEIDNVMHANYLFWRNS
Consensus (7216)		NASSEAF	LIGINYLG	----	KPKVEIDNVMHANYLFWRNS

**FIGURE 4A (contd.)**

							Section 187
	(7255)	7255	7260	7270	7280	7293	
avian infectious bronchitis pol 1ab (6565)	NYLQTS	AYSL	EDVAK	EDLR	KATP	VNLKTEOKTDEL	FN
bovine coronavirus pol 1ab (7030)	TVWNGG	AYSL	EDMAK	PLKLAG	AVENLR	ADQINDM	YS
Human corona 229E pol 1ab (6694)	TVMSLS	SYNS	VLLDLS	KENCKH	KATV	VQIKDSDINEM	VLS
Murine hepatitis pol 1ab (7114)	TMWNGG	AYSL	EDMS	PLKAAG	TAVVSI	KPDQINDL	VLS
Consensus (7255)	TVWNGS	AYS	LFDMAK	EPLK	LKATAV	VNLK	DQINDLVLS
							Section 188
	(7294)	7294	7300	7319			
avian infectious bronchitis pol 1ab (6604)	LIEKCG	KLLVR	DVGNT	SETSDS	SVCTM	SEQ ID NO: 9905	
bovine coronavirus pol 1ab (7069)	LIEKGG	KLLVR	DTNKE	VEVGD	SLVNV	SEQ ID NO: 9886	
Human corona 229E pol 1ab (6733)	LVRSEN	LEVRG	NGKCL	SFSN	HEVSTK	SEQ ID NO: 9914	
Murine hepatitis pol 1ab (7153)	LIEKGG	KLLVR	DTNKE	VEVGD	SLVNVK	SEQ ID NO: 9887	
Consensus (7294)	LIEKGG	KLLVR	DTGKE	VFVSD	SLVNVK		

**FIGURE 4B**

		Section 1				
		(1)	1	10	20	39
human coronavirus OC43 NP	(1)	MSFTPGKQSSS	-RAS	SGNRSGNGILK	---	WADQSDQVRN
Bovine corona NP	(1)	MSFTPGKQSSS	-RAS	SGNRSGNGILK	---	WADQSDQSRN
avian infectious bronchitis virus NP	(1)	-----	MA	SKAAG	--K	SSP--AP-
mouse hepatitis virus NP	(1)	MSFVPGQEN	AGGRSS	SVNRAGN	CTLKKT	TWADQTERGPN
Consensus	(1)	MSFTPGKQSSS	RASSGN	RSNGILK		WADQSDQARN
		Section 2				
		(40)	40	50	60	78
human coronavirus OC43 NP	(36)	VQTRGRRAQ	PKQTATSQ	PSGGNVV	PPYY	WESGLTQFQK
Bovine corona NP	(36)	VQTRGRRAQ	PKQTATSQ	PSGGNVV	PPYY	WESGLTQFQK
avian infectious bronchitis virus NP	(16)	LIKLG	GPKPKV	GSSGN	-----	ASNECAI
mouse hepatitis virus NP	(40)	NONRGRNON	PKQTATIQ	-PNSGS	VVDHY	WESGLTQFQK
Consensus	(40)	VQTRGRRAQ	PKQTATSQ	PSGGNVV	PPYY	SWFSGITQFQK
		Section 3				
		(79)	79	90	100	117
human coronavirus OC43 NP	(75)	GKEEFV	QCP	TIAPGV	PATEAK	YVYHN
Bovine corona NP	(75)	GKEEFV	QCP	TIAPGV	PATEAK	YVYHN
avian infectious bronchitis virus NP	(45)	NAPAPKF	ECSEV	DNEN	EKNSQ	Q
mouse hepatitis virus NP	(78)	GKEEFQF	Q	V	TIANGIP	ASEQK
Consensus	(79)	GKEFEFAEGQGVPIAPGV	PASEQ	KGYWYRHN	RRS	FKTAD
		Section 4				
		(118)	118	130	140	156
human coronavirus OC43 NP	(114)	GNORQLLPRWYFY	YLG	TGPHAK	DQY	TDID
Bovine corona NP	(114)	GNORQLLPRWYFY	YLG	TGPHAK	DQY	TDID
avian infectious bronchitis virus NP	(82)	GGRKPM	PDAL	TTT	STAD	LNW
mouse hepatitis virus NP	(117)	QOKODLPRWYFY	YLG	TGPH	GASY	ODS
Consensus	(118)	GNQKQLLPRWYFY	YLG	TGPHAK	DQY	GTSID
		Section 5				
		(157)	157	170	180	195
human coronavirus OC43 NP	(153)	ADVNT	RADIVDRDP	SSDEAI	PT	PP
Bovine corona NP	(153)	ADVNT	RADILD	SSDEAI	PT	PP
avian infectious bronchitis virus NP	(121)	AVKSR	SNQGT	PDCK	NFDQY	LR
mouse hepatitis virus NP	(156)	ADVNT	RS	DIVE	SS	DEAI
Consensus	(157)	ADVNT	RADIVDRDP	SSDEAI	PT	PP
		Section 6				
		(196)	196	210	220	234
human coronavirus OC43 NP	(189)	EGSG	APNSRST	RTS	ASSAG	SRSRANS
Bovine corona NP	(189)	EGSG	APNSRST	RAS	ASSAC	SRSRANS
avian infectious bronchitis virus NP	(160)	LSR	GR	STAAS	AAS	RV
mouse hepatitis virus NP	(192)	EGSG	APASR	SG	RS	G
Consensus	(196)	EGSG	RSAPNSRST	SRASSR	ASSAG	SRSRANS

**FIGURE 4B (contd.)**

Section 7

	(235)	235	240	250	260	273																																		
human coronavirus OC43 NP (228)		VT	PDMA	DQIASLVLAKLGKDATK	PQOVTH	EAKVROKI																																		
Bovine corona NP (228)		VT	PDMA	DQIASLVLAKLGKDATK	PQOVTK	OTAKEIROKI																																		
avian infectious bronchitis virus NP (192)		A	E	D	L	I	A	A	A	I	T	Q	D	Q	---	R	K	G	T	P	E	T	K	Q	A	E	E	M	A	H	R	R								
mouse hepatitis virus NP (229)		M	K	P	D	M	A	E	E	I	A	L	V	L	A	K	L	G	K	D	A	G	O	P	K	O	V	I	K	O	S	I	K	V	R	O	K	I		
Consensus (235)		V	T	P	D	M	A	D	Q	I	A	S	L	V	L	A	K	L	G	K	D	A	T	K	P	Q	O	V	T	K	O	T	A	K	E	V	R	O	K	I

Section 8

	(274)	274	280	290	300	312																																	
human coronavirus OC43 NP (267)		L	N	K	P	R	O	K	R	S	P	N	K	O	C	T	V	Q	O	C	F	G	K	R	G	P	N	O	--	N	F	G	G	G	E	M	L	K	L
Bovine corona NP (267)		L	N	K	P	R	O	K	R	S	P	N	K	O	C	T	V	Q	O	C	F	G	K	R	G	P	N	O	--	N	F	G	G	G	E	M	L	K	L
avian infectious bronchitis virus NP (227)		E	C	K	---	---	---	---	K	T	V	P	P	G	Y	R	V	D	V	T	G	P	P	T	K	G	R	E	G	N	T	G	D	D	K	K	N	E	E
mouse hepatitis virus NP (268)		L	N	K	P	R	O	K	R	S	P	N	K	O	C	T	V	Q	O	C	F	G	K	R	G	P	N	O	--	N	F	G	G	E	M	L	K	L	
Consensus (274)		L	N	K	P	R	O	K	R	S	P	N	K	O	C	T	V	Q	O	C	F	G	K	R	G	P	N	O	--	N	F	G	G	E	M	L	K	L	

Section 9

	(313)	313	320	330	340	351																																	
human coronavirus OC43 NP (304)		G	T	S	D	P	Q	F	P	I	L	A	E	L	A	P	T	A	G	A	F	F	F	G	S	R	L	E	L	A	K	V	O	N	-----				
Bovine corona NP (304)		G	T	S	D	P	Q	F	P	I	L	A	E	L	A	P	T	A	G	A	F	F	F	G	S	R	L	E	L	A	K	V	O	N	-----				
avian infectious bronchitis virus NP (262)		G	I	K	D	G	R	V	T	A	M	L	N	T	T	S	P	H	A	C	L	T	O	G	R	V	T	P	K	L	Q	P	D	G	L	H	L	R	F
mouse hepatitis virus NP (305)		G	T	S	D	P	Q	F	P	I	L	A	E	L	A	P	T	V	G	A	E	E	T	S	A	K	L	E	E	V	K	K	N	-----					
Consensus (313)		G	T	S	D	P	Q	F	P	I	L	A	E	L	A	P	T	A	G	A	F	F	F	G	S	R	L	E	L	A	K	V	O	N					

Section 10

	(352)	352	360	370	380	390																																
human coronavirus OC43 NP (337)		---	L	S	G	N	P	D	E	P	O	K	D	V	E	L	R	Y	N	G	A	I	R	E	D	S	T	L	S	G	F	E	T	I	M	K	V	
Bovine corona NP (337)		---	L	S	G	N	L	D	E	P	O	K	D	V	E	L	R	Y	N	G	A	I	R	E	D	S	T	L	S	G	F	E	T	I	M	K	V	
avian infectious bronchitis virus NP (301)		E	F	T	T	V	P	R	E	D	P	O	F	I	N	V	K	I	C	D	E	C	M	D	G	V	G	E	R	P	K	D	E	V	V	R	P	K
mouse hepatitis virus NP (337)		---	S	G	A	D	E	P	T	K	E	V	M	E	L	O	Y	S	G	A	V	R	E	D	S	L	E	G	F	E	T	I	M	K	V			
Consensus (352)		---	L	S	G	N	P	D	E	P	O	K	D	V	E	L	R	Y	N	G	A	I	R	E	D	S	T	L	S	G	F	E	T	I	M	K	V	

Section 11

	(391)	391	400	410	429																															
human coronavirus OC43 NP (373)		L	N	E	N	L	N	A	Y	Q	Q	D	G	M	M	N	S	P	K	P	O	R	G	H	K	N	G	Q	---	G	E	N	D	N		
Bovine corona NP (373)		L	N	E	N	L	N	A	Y	Q	Q	D	G	M	M	N	S	P	K	P	O	R	G	O	K	N	G	Q	---	G	E	N	D	N		
avian infectious bronchitis virus NP (340)		S	R	P	N	S	---	R	P	A	T	R	T	S	S	P	A	P	R	O	R	O	K	K	E	K	S	E	---	K	O	D	D	E		
mouse hepatitis virus NP (372)		L	N	E	N	L	N	A	Y	Q	Q	D	G	C	A	D	V	M	S	P	K	P	O	R	G	R	R	O	A	O	E	K	K	E	V	N
Consensus (391)		L	N	E	N	L	N	A	Y	Q	Q	D	G	M	M	N	S	P	K	P	O	R	O	K	G	K	N	G	Q	---	G	E	N	D	N	

Section 12

	(430)	430	440	450	468																																
human coronavirus OC43 NP (409)		I	S	V	A	P	K	S	R	V	Q	O	N	K	S	R	E	L	T	A	E	D	I	S	L	L	K	K	M	D	E	P	-----	Y	T		
Bovine corona NP (409)		I	S	V	A	P	K	S	R	V	Q	O	N	K	S	R	E	L	T	A	E	D	I	S	L	L	K	K	M	D	E	P	-----	Y	T		
avian infectious bronchitis virus NP (373)		M	D	K	A	L	T	S	D	E	E	R	N	I	---	A	O	E	F	D	E	P	K	V	I	N	W	G	D	S	-----	A					
mouse hepatitis virus NP (410)		I	S	V	A	P	K	S	S	V	O	R	N	V	S	R	E	L	T	P	E	D	R	S	L	L	A	O	L	D	D	G	V	P	D	G	L
Consensus (430)		I	S	V	A	P	K	S	R	V	Q	O	N	K	S	R	E	L	T	A	E	D	I	S	L	L	K	K	M	D	D	P	-----	Y	T		

Section 13

	(469)	469	474					
human coronavirus OC43 NP (443)		E	D	T	S	E	I	SEQ ID NO: 9915
Bovine corona NP (443)		E	D	T	S	E	I	SEQ ID NO: 9887
avian infectious bronchitis virus NP (404)		L	C	E	N	E	L	SEQ ID NO: 9906
mouse hepatitis virus NP (449)		E	D	D	S	N	V	SEQ ID NO: 9898
Consensus (469)		E	D	T	S	E	I	

**FIGURE 4C**

Section 1						
	(1)	10	20	30	42	
human coronavirus OC43 HE	(1)	----	MELLPRFILVSCIIGSLGFIYRRTNVAIVNGENEEFG			
bovine coronavirus HE	(1)	----	MFLLLRFVLVSCIIGSLGFDNPPTNVVSHLNGEWFEEFG			
mouse hepatitis virus HE	(1)	MARTDAMAEPTLEFLVLSLGYAFGENEELLVVSHLNDDEEFG				
Consensus	(1)		MFLLPREFILVSCIIGSLGFENPPTNVVSHLNGDWELFG			
Section 2						
	(43)	43	50	60	70	84
human coronavirus OC43 HE	(39)	DSRSDCNHIVNINP	NYSYMDLNPVLCDSGKISSKAGNSIFR			
bovine coronavirus HE	(39)	DSRSDCNHIVNTNPRNYS	MEENPALGDSGKISSKAGNSIFR			
mouse hepatitis virus HE	(43)	DSRSDCNHINNLSQQN	NYHDIPELCKSAKISSAFAENSLEK			
Consensus	(43)	DSRSDCNHIVNINP	NYSYMDLNP	LCDSGKISSKAGNSIFR		
Section 3						
	(85)	85	90	100	110	126
human coronavirus OC43 HE	(81)	SEHETDFYNYTGE	GQQIFIEGVNFTPYHAFKCNRS	SGSNDIW		
bovine coronavirus HE	(81)	SEHETDFYRYTGE	GQQIFIEGLNFTPYHAFKCTTS	SGSNDIW		
mouse hepatitis virus HE	(85)	SEHETDFYNYTGE	SSQIFIEGVNFTPYVGLNNNDNRW			
Consensus	(85)	SEHETDFYNYTGE	GQQIIFYEGVNETPYHAFKC	SGSNDIW		
Section 4						
	(127)	127	140	150	168	
human coronavirus OC43 HE	(123)	MQNKGLFYTQVYKNMAVYRSLTFVNVPYVYNGSAQSTALCKS				
bovine coronavirus HE	(123)	MQNKGLFYTQVYKNMAVYRSLTFVNVPYVYNGSAQSTALCKS				
mouse hepatitis virus HE	(127)	MGNKARFYTQVYKNMAHXSNSVGNITTYNGGAGVSMCKH				
Consensus	(127)	MQNKGLFYTQVYKNMAVYRSLTFVNVPYVYNGSAQSTALCKS				
Section 5						
	(169)	169	180	190	200	210
human coronavirus OC43 HE	(165)	GS----	LVLNNPAYIAPQANSGLVYKVFADFYLSGCDYIV			
bovine coronavirus HE	(165)	GS----	LVLNNPAYIAREANFGDIYKVFADFYLSGCDYIV			
mouse hepatitis virus HE	(169)	IANGVTITLNNTTETISKEVSKPQYVYESGANYTLOCGDEIV				
Consensus	(169)	GS	LVLNNPAYIAKEAN	GDYYYKVEADFYLSGCDYIV		
Section 6						
	(211)	211	220	230	240	252
human coronavirus OC43 HE	(203)	PLCIFNGKFLSNTKYYDDSQYYFNKDTGVIYGLNSTETITTTG				
bovine coronavirus HE	(203)	PLCIFNGKFLSNTKYYDDSQYYFNKDTGVIYGLNSTETITTTG				
mouse hepatitis virus HE	(211)	PLCYFNGQKSSKLYDPSQAYKXVDTCVLYGTNGLNLTSS				
Consensus	(211)	PLCIFNGKFLSNTKYYDDSQYYFNKDTGVIYGLNSTETITTTG				
Section 7						
	(253)	253	260	270	280	294
human coronavirus OC43 HE	(245)	EDLNCYHYLVLP	SGNYLAISNELLITVPTKAICLNKRKDFTPV			
bovine coronavirus HE	(245)	EDPNCHYLVLP	SGNYLAISNELLITVPTKAICLNKRKDFTPV			
mouse hepatitis virus HE	(253)	LDLTCIYVAITPCNYVES	QNHGILVYSKALGLRPKALHLV			
Consensus	(253)	FDLNCHYLVLP	SGNYLAISNELLITVPTKAICLNKRKDFTPV			

**FIGURE 4C (contd.)**

Section 8						
	(295)	295	300	310	320	336
human coronavirus OC43 HE (287)		QVVD	SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN			
bovine coronavirus HE (287)		QVVD	SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN			
mouse hepatitis virus HE (295)		QVVD	SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN			
Consensus (295)		QVVD	SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN			
Section 9						
	(337)	337	350	360	378	
human coronavirus OC43 HE (329)		HGDAGFTSILSGLLYNSPCFSQQGVFRYDNVSSVWPPLYPYGR				
bovine coronavirus HE (329)		HGDAGFTSILSGLLYNSPCFSQQGVFRYDNVSSVWPPLYPYGR				
mouse hepatitis virus HE (337)		HGDAGFTSILSGLLYNSPCFSQQGVFRYDNVSSVWPPLYPYGR				
Consensus (337)		HGDAGFTSILSGLLYNSPCFSQQGVFRYDNVSSVWPPLYPYGR				
Section 10						
	(379)	379	390	400	410	420
human coronavirus OC43 HE (371)		CPTAADINPDLPICVYDPLPVILLGILLGVAVIIIVVLLLY				
bovine coronavirus HE (371)		CPTAADINPDLPICVYDPLPVILLGILLGVAVIIIVVLLLY				
mouse hepatitis virus HE (379)		CPTAADINPDLPICVYDPLPVILLGILLGVAVIIIVVLLLY				
Consensus (379)		CPTAADINPDLPICVYDPLPVILLGILLGVAVIIIVVLLLY				
Section 11						
	(421)	421	432			
human coronavirus OC43 HE (413)		FMVDNGTRLHDA		SEQ ID NO: 9916		
bovine coronavirus HE (413)		FMVDNGTRLHDA		SEQ ID NO: 9888		
mouse hepatitis virus HE (420)		FMVDNGTRLHDA		SEQ ID NO: 9899		
Consensus (421)		FMVDNGTRLHDA				

**FIGURE 4D**

Section 1					
	(1)	1	10	20	39
bovine coronavirus Sm	(1)	MFMA	ADAYFADTVWYVGQIIFIVAICLLVII	--	VVVAFLA
avian infectious bronchitis virus Sm	(1)	MNEL	NKSLEEENGSELTAYIIVGFLAYLLGRALQ		IVQ
mouse hepatitis virus Sm	(1)	--MF	NLEITDTVWYVGQIIFFAVGLMVTI	--	IVVAFLA
Consensus	(1)	M M N	FL DTVWYVGQIIFIVAICLLVII		IVVAFLA
Section 2					
	(40)	40	50	60	78
bovine coronavirus Sm	(38)	IFKLC	IQLCGMNTLVLSPSIYVENRGEOFYF		DK
avian infectious bronchitis virus Sm	(40)	AADA	CLFWYTWVHPGAKGTAFVYKTYGRKLN		PEE
mouse hepatitis virus Sm	(36)	SIKLC	IQLCGMNTLVLSPSIYLYDRSKOLYKY		PEE
Consensus	(40)	S KLCI	QLCGMNTLVLSPSIYLF R KQ YKFYN		ELK
Section 3					
	(79)	79	90	108	
bovine coronavirus Sm	(76)	PPVLD	VDDI		SEQ ID NO: 9889
avian infectious bronchitis virus Sm	(79)	AVIVN	EFPKNGWNNKNPANFQDAQRDKLYS		SEQ ID NO: 9907
mouse hepatitis virus Sm	(75)	LPVLD	VDDI		SEQ ID NO: 9900
Consensus	(79)	PILD	VDDI		

**FIGURE 4E**

		Section 1				
		(1)	10	20	30	40
human coronavirus OC43 M	(1)	-MSSKTPAPVYIWTADEAIFKFLKEWNFSLGIILLFITII				
bovine coronavirus M	(1)	-MSSVTPAPVYIWTADEAIFKFLKEWNFSLGIILLFITII				
avian infectious bronchitis virus M	(1)	-----MSNAANCTLDCEQSVELFLEKRLFITAFLLFTIID				
mouse hepatitis virus M	(1)	MTSTTQAPQPVYQWTADEAIFKFLKEWNFSLGIILLFITII				
Consensus	(1)	MSS TTPAPVYIWTADEAIFKFLKEWNFSLGIILLFITII				
		Section 2				
		(41)	41	50	60	70
human coronavirus OC43 M	(40)	LLEFYPSRSMFVYVIMLLEWLMARLTIIITIFNCVYALN				
bovine coronavirus M	(40)	LLEFYTSIMFVYVIMLLEWLMARLTIIITIFNCVYALN				
avian infectious bronchitis virus M	(36)	LQYIATSRRTFMNIVLWCFWELNIAMGVISCTPPN				
mouse hepatitis virus M	(41)	LLEFYPSRSMFVYVIMLLEWLMARLTIIITIFNCVYALN				
Consensus	(41)	LQFGYTSRSMFVYVIMLLEWLMARLTIIITIFNCVYALN				
		Section 3				
		(81)	81	90	100	110
human coronavirus OC43 M	(80)	NVYLGSLVFTIVAIIMWIVFVNSIRLFIRTGSWWSFNP				
bovine coronavirus M	(80)	NVYLGSLVFTIVAIIMWIVFVNSIRLFIRTGSWWSFNP				
avian infectious bronchitis virus M	(76)	TGGVAAKLLIVACLSFEGWIOQLRDKRGOWWALNP				
mouse hepatitis virus M	(81)	NVYLGSLVFTIVAIIMWIVFVNSIRLFIRTGSWWSFNP				
Consensus	(81)	NVYLGSLVFTIVAIIMWIVFVNSIRLFIRTGSWWSFNP				
		Section 4				
		(121)	121	130	140	150
human coronavirus OC43 M	(120)	ETNNLMCIDMKGTMYVRPIIEDYHTLTVTIIRGHLYMOGI				
bovine coronavirus M	(120)	ETNNLMCIDMKGRMYVRPIIEDYHTLTVTIIRGHLYMOGI				
avian infectious bronchitis virus M	(116)	SSIAVGSLLESLNGQOCNFALESVPMVLSPLIKNGVLYCEG				
mouse hepatitis virus M	(121)	ETNNLMCIDMKGTMYVRPIIEDYHTLTVTIIRGHLYMOGI				
Consensus	(121)	ETNNLMCIDMKGTMYVRPIIEDYHTLTVTIIRGHLYMOGI				
		Section 5				
		(161)	161	170	180	190
human coronavirus OC43 M	(160)	KLGTGYSLSDLPAYVTVAKVSHLCTYKRGFLDKIDTSGE				
bovine coronavirus M	(160)	KLGTGYSLSDLPAYVTVAKVSHLCTYKRGFLDKIDTSGE				
avian infectious bronchitis virus M	(156)	QWLAKCEPDHLEKDTIFCPPDRNIR-----MV				
mouse hepatitis virus M	(161)	KLGTGYSLSDLPAYVTVAKVSHLCTYKRGFLDKIDTSGE				
Consensus	(161)	KLGTGYSLSDLPAYVTVAKVSHLCTYKRGFLDKIDTSGE				
		Section 6				
		(201)	201	210	220	230
human coronavirus OC43 M	(200)	AVYVSKVGNRYRLPSTQKSGMDTALLRNNI				
bovine coronavirus M	(200)	AVYVSKVGNRYRLPSTQKSGMDTALLRNNI				
avian infectious bronchitis virus M	(185)	QKVTGDOSENKKRFAT-----				
mouse hepatitis virus M	(201)	AVYVSKVGNRYRLPSN-KPSGMDTALLRI--				
Consensus	(201)	AVYVSKVGNRYRLPSTQKSGMDTALLRNNI				

SEQ ID NO: 9917  
 SEQ ID NO: 9890  
 SEQ ID NO: 9908  
 SEQ ID NO: 9901

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**FIGURE 4F**

Section 1									
	(1)	10	20	30	40				
human coronavirus OC43 S	(1)	MELILLISLPTAF	AVIGDLKCTSDN	-INDKDTGPP	PTSTD				
avianinfectiousbronchitisvirusS	(1)	-----	-----	-----	-----				
bovine coronavirus S	(1)	MELILLISLPTAF	AVIGDLKCTTVS	-INDVDTGVP	PSISTD				
mouse hepatitis virus S	(1)	MLEMFLFLFPSC	IGYIGDFRCIC	LVNSNGANV	FAPSTSTE				
Consensus	(1)	MELILLISLPTAF	AVIGDLKCTSL	IND DTG	PSISTD				
Section 2									
	(41)	41	50	60	70	80			
human coronavirus OC43 S	(40)	TVDVTNGLGTY	YVLDRVYLN	TLLFNGY	YPTSG	STYRNMA			
avianinfectiousbronchitisvirusS	(1)	-----	-----	MLVPL	LLVTL	LCLCSAVLYD			
bovine coronavirus S	(40)	TVDVTNGLGTY	YVLDRVYLN	TLLFNGY	YPTSG	STYRNMA			
mouse hepatitis virus S	(41)	TVEVSQGLGTY	YVLDRVYLN	ATLTLTG	YYPVD	GSKFRNDA			
Consensus	(41)	TVDVTNGLGTY	YVLDRVYLN	TLLFNGY	YPTSG	STYRNMA			
Section 3									
	(81)	81	90	100	110	120			
human coronavirus OC43 S	(80)	LKGSVLLSRLW	KKFELSDF	INGTEAK	VKN	TKVTKDRVMY			
avianinfectiousbronchitisvirusS	(23)	SSSYVYYYQSA	HRFSGWHL	QCCAY	VANIS	SEFNNAGSS			
bovine coronavirus S	(80)	LKGTLLLSLTL	WKKFELSDF	RTNTEAK	VKN	TKVTKDQVMY			
mouse hepatitis virus S	(81)	LTGTNSVLSL	WTCQPYLSQ	ENDCTFAK	VON	LKTSTPSGAT			
Consensus	(81)	LKGTVLLS	SWFKPP	FELSDF	NNGIFAK	VKN	TKVIKDAVMY		
Section 4									
	(121)	121	130	140	150	160			
human coronavirus OC43 S	(120)	SEFPATITG	SSTFVNTS	YSV	VVQ	ORTINSTQDGNK	LOGLL		
avianinfectiousbronchitisvirusS	(63)	SGCTVGIT	HGGRVVN	ASSI	AMTAP	-----	-----		
bovine coronavirus S	(120)	SEFPATITG	SSTFVNTS	YSV	VVQ	-----	HTTILGNKLOGLE		
mouse hepatitis virus S	(121)	AYEPFIV	GSLEGYTS	ETV	VLEP	-----	YNG-----VY		
Consensus	(121)	SEFPATITG	SSTFVNTS	YSV	VVQ	T	GNKLOGLL		
Section 5									
	(161)	161	170	180	190	200			
human coronavirus OC43 S	(160)	EMVVCQYNM	CEYPOTTCH	PNLG-NHR	KELI	WHLDTCGVV	SCL		
avianinfectiousbronchitisvirusS	(88)	--	GMAWSSSE	ECTAH	NFS	DTTVEVTHC	AKHGGCPLTGM		
bovine coronavirus S	(156)	ET	VCQYTMCE	YNTTIC	PNLG-NQ	RELWH	WDTCGVV	SCL	
mouse hepatitis virus S	(149)	MA	VCQYTM	ICLLPY	IDCK	PNTNG	NKLIG	WHTEVKPPICV	
Consensus	(161)	EISVCQYTM	CEYPNTTIC	PNLG	N	RIELWH	DTGVV	SCL	
Section 6									
	(201)	201	210	220	230	240			
human coronavirus OC43 S	(199)	MKRNETY	DVNADY	LYFHFYQ	EGGTE	FAYFT	DTGVVTK	KELE	
avianinfectiousbronchitisvirusS	(126)	LQONLIR	VSAMNG	QLFY	NLT	VS	VAKYPT	ERSFQC	VNNIT
bovine coronavirus S	(195)	YKRNETY	DVNADY	LYFHFYQ	EGGTE	FAYFT	DTGVVTK	KELE	KELE
mouse hepatitis virus S	(189)	LKR	ETLNV	NADAFY	FHFYQ	HGGTE	FAYAY	ADKPS	ATTELE
Consensus	(201)	YKRNETY	DVNADY	LYFHFYQ	EGGTE	FAYFT	DTGVVTK	KELE	KELE



**FIGURE 4F (contd.)**

Section 7						
	(241)	241	250	260	270	280
human coronavirus OC43 S	(239)	NVYLGMALSHYYVMPLTCN----	SKLTLEYWVTPLTSTRQY			
avianinfectiousbronchitisvirusS	(166)	SVYLDNGDLYVTSNETIDVTSAGVYFKAGGPITYKVMREVK				
bovine coronavirus S	(235)	NVYLIGTMLSHYYVMPLTCN----	SALTLEYWVTPLTSTRQY			
mouse hepatitis virus S	(229)	SVYLIGDILLYVLEPTICNPTAGSTFAPRYWVTPLTSTRQY				
Consensus	(241)	SVYLGILSHYYVMPLTCN	A S	LTLEYWVTPLTSTRQY		
Section 8						
	(281)	281	290	300	310	320
human coronavirus OC43 S	(275)	LLAFNODDITFENAEDCMSDFMSEIKCKTQSIAPPTGVYEL				
avianinfectiousbronchitisvirusS	(206)	ALAYFVNQTAQDVLLDCSPRGLHACQYNTGNFSDGFPE				
bovine coronavirus S	(271)	LLAFNODGVIFNAVDCKSDFMSEIKCKTILSIAPSTGVYEL				
mouse hepatitis virus S	(269)	LFNENQKGVITSAVDCASSYTSEIKCKTOSMLRSTGVYEL				
Consensus	(281)	LLAFNQDGVIFNAVDC	SSFMSEIKCKTQSIAPSTGVYEL			
Section 9						
	(321)	321	330	340	350	360
human coronavirus OC43 S	(315)	NGYTVQPIADVYRKKNLPLNCNIEAWLNDKSVPSPLNWER				
avianinfectiousbronchitisvirusS	(246)	TNSSLVKQKFFVYR-----	NSVNTTCTLHNFIEHN			
bovine coronavirus S	(311)	NGYTVQPIADVYRIPNLPDGNIEAWLNDKSVPSPLNWER				
mouse hepatitis virus S	(309)	SGYTVQPIADVYRANLPACNIEAWLTARSVPSPINWER				
Consensus	(321)	NGYTVQPIADVYRRIPNLP	CNIEAWLNDKSVPSPLNWER			
Section 10						
	(361)	361	370	380	390	400
human coronavirus OC43 S	(355)	KTFENCNFNMSLSLMSFIQADSFCTCNNIDAAKIYGMCFSSI				
avianinfectiousbronchitisvirusS	(277)	ETGALPNP-----	SGVNIQTYQTKTAQSGYNNFN	SFL		
bovine coronavirus S	(351)	KTFENCNFNMSLSLMSFIQADSFCTCNNIDAAKIYGMCFSSI				
mouse hepatitis virus S	(349)	KTFENCNFNMSLSLRYVGAESLFCNNIDAASKVYGRCECST				
Consensus	(361)	KTFENCNFNMSLSLMSFIQADSFCTCNNIDAAKIYGMCFSSI				
Section 11						
	(401)	401	410	420	430	440
human coronavirus OC43 S	(395)	TIDKFAIPNGRKVDLQGLNLGYLQSFNYRIDTTATSCQLY				
avianinfectiousbronchitisvirusS	(311)	SSFVYKESNFMYGSYHPCKFRETTINGHWFNLSLVSTHA				
bovine coronavirus S	(391)	TIDKFAIPNGRKVDLQGLNLGYLQSFNYRIDTTATSCQLY				
mouse hepatitis virus S	(389)	SYDKFAVPNSROVDLQGLNSGFQTA YRIDTAATSCQLH				
Consensus	(401)	SIDKFAIPNGRKVDLQGLNLGYLQSFNYRIDTTATSCQLY				
Section 12						
	(441)	441	450	460	470	480
human coronavirus OC43 S	(435)	YNLPAANVSVSRRFPSTWNRREGFIEDSVEKPPAPAGVLIN				
avianinfectiousbronchitisvirusS	(351)	YGP-----	LOG-----			
bovine coronavirus S	(431)	YNLPAANVSVSRRFPSTWNRREGFETQSVEKPPAPAGVFTD				
mouse hepatitis virus S	(429)	YTLRKNNVTINNHNPSWNRRYGENDACVEGKN-----Q				
Consensus	(441)	YNLPAANVSVSRRFPSTWNRREGF	E	SVEKPPAPAGV	TN	

**FIGURE 4F (contd.)**

						Section 13
	(481)	481	490	500	510	520
human coronavirus OC43 S	(475)	HDVVYAQHCFKAPKNEPCKLNG-SCVGS	GP-----	GKNN		
avianinfectiousbronchitisvirusS	(357)	---GCKQSVFKGRATCCYAYSYG	GPSLCKKGVYSG-----			
bovine coronavirus S	(471)	HDVVYAQHCFKASINFCPCKLDGSL	VGNGPGIDAGYKTS			
mouse hepatitis virus S	(463)	HDVVYAQQCTTVRSYYCPCAQPD	IVSPCITQTK-----	P		
Consensus	(481)	HDVVYAQHCFKARSNFCPCKL	G LSVGS	GP		K
						Section 14
	(521)	521	530	540	550	560
human coronavirus OC43 S	(509)	GIGTCPAGTNYLTCDN-----	LCTPDPIT--	FTGT	YKCP	
avianinfectiousbronchitisvirusS	(388)	-----				
bovine coronavirus S	(511)	GIGTCPAGTNYLTCHNAAQCDC	LCTPDPIT	SKATG	PYKCP	
mouse hepatitis virus S	(497)	-----				
Consensus	(521)	GIGTCPAGTNYLTC	N	LCTPDPIT	TG	YKCP
						Section 15
	(561)	561	570	580	590	600
human coronavirus OC43 S	(541)	QTKSLVGIGEHSGIAVKSDYCG	-----	GNSCTCR	POAFLG	
avianinfectiousbronchitisvirusS	(388)	----EILDHNFEGLEVVYTKSGG	-----			
bovine coronavirus S	(551)	QTRYDVGIGEHSGIAVKSDHCG	-----	GNPCTCQ	POAFLG	
mouse hepatitis virus S	(497)	-KSAFMYVGDHCEGEGVLEDC	GNADPHKGCICANN	SPFG		
Consensus	(561)	QTKALVGIGEHCSGLAVKSDHCG		GN	CTC	POAFLG
						Section 16
	(601)	601	610	620	630	640
human coronavirus OC43 S	(577)	WSADSCLOGDRCNIFANFILH	DVNSGLTCTD	LQKANTDI		
avianinfectiousbronchitisvirusS	(407)	-----	SR-LOTATE	PEFVITANNYNN		
bovine coronavirus S	(587)	WSVDSCLOGDRCNIFANFILH	DVNSGTTCTD	LQKSN	TDI	
mouse hepatitis virus S	(536)	WSHDTCLVNDRCQITANILL	NGINSGTTCTD	LQLP	NTEV	
Consensus	(601)	WS	DSCLQGDRCNIFANFILHD	INSGTTCTD	LQKANTDI	
						Section 17
	(641)	641	650	660	670	680
human coronavirus OC43 S	(617)	ILGVGVNYDLYGITGQGITVE	VNATYYNSWQNL	LYDSNGN		
avianinfectiousbronchitisvirusS	(427)	TENTCVDNNIYGRTEGCTT	INZTDSAVS--	YNYLA	AGLA	
bovine coronavirus S	(627)	ILGVGVNYDELGITGQGLE	VNATYYNSWQNL	LYDSNGN		
mouse hepatitis virus S	(576)	VTGTCVNYDLYGITGQGV	FKEVKADLYNSWQ	LLYDVNGN		
Consensus	(641)	ILGVGVNYDLYGITGQGIT	VEVNATYYNSWQNL	LYDSNGN		
						Section 18
	(681)	681	690	700	710	720
human coronavirus OC43 S	(657)	LYGFRDYITNRTFMIRSCY	SGRVSAAFHANS	SEBALLERN		
avianinfectiousbronchitisvirusS	(465)	ELDTSCSIDIFVVQGEYGL	NYKVNPCEDVN	QFVMSGGK		
bovine coronavirus S	(667)	LYGFRDYITNRTFMIRSCY	SGRVSAAFHANS	SEBALLERN		
mouse hepatitis virus S	(616)	LNGFRDLTTNKTYTIRSCY	SGRVSAAFHKA	EPALBYRN		
Consensus	(681)	LYGFRDYITNRTFMIRSCY	SGRVSAAFHANS	SEBALLERN		

**FIGURE 4F (contd.)**

Section 19						
	(721)	721	730	740	750	760
human coronavirus OC43 S	(697)	IKCNYVFENN	SLSRQLQPINY	FDSYLGCVVN	AYNSTAI	SVQ
avianinfectiousbronchitisvirusS	(505)	EVGILTSRNET	GSQLENDQY	IKITNGTRR	FRRSITEN	VVA
bovine coronavirus S	(707)	IKCNYVFENN	TLRQLQPINY	FDSYLGCVVN	ADNSTSS	SVQ
mouse hepatitis virus S	(656)	INC SYVES	HNISREENP	ENYFDSYLG	CVVNADNR	TDENP
Consensus	(721)	IKCNYVFENN	SLSRQLQPINY	FDSYLGCVVN	ADNSTSE	AVQ
Section 20						
	(761)	761	770	780	790	800
human coronavirus OC43 S	(737)	TCDLTVGSGY	CVDYSKNRR	SRGAITTG	YRFTNNE	PFTVNS
avianinfectiousbronchitisvirusS	(545)	NEPYVSYCKE	ELKPDG	-----	SIATIVE	KQL
bovine coronavirus S	(747)	TCDLTVGSGY	CVDYSTKR	RSRSITTG	YRFTNNE	PFTVNS
mouse hepatitis virus S	(696)	NCDLRMGAG	LCVDYSKSR	RAIRSYST	GYRLTTE	FPPTML
Consensus	(761)	TCDLTVGSGY	CVDYSK	RRSRSIT	TGYRFTN	FEPTVNS
Section 21						
	(801)	801	810	820	830	840
human coronavirus OC43 S	(777)	VNDSLEPVGG	LYEIQTISE	TTIGNMV	EFCTSSP	AVTDC
avianinfectiousbronchitisvirusS	(571)	EQFVAPLFN	VNTENML	LENSNLT	VTDTYIT	OTRMDIQ
bovine coronavirus S	(787)	VNDSLEPVGG	LYEIQTISE	TTIGNME	EFCTSSP	AVTDC
mouse hepatitis virus S	(736)	VNDSVCS	VDGLYEMQ	PTNTTIG	HEEEIT	TRSPKTY
Consensus	(801)	VNDSLEPVGG	LYEIQIP	SEFTTIGN	MEEFIQT	SSPKVTIDC
Section 22						
	(841)	841	850	860	870	880
human coronavirus OC43 S	(817)	AAFWCGDYA	ACKSOLVE	YGSFCDN	INAILTE	VNELLD
avianinfectiousbronchitisvirusS	(611)	LQVACGSS	LDNRKLF	QQSGPV	LDNLSV	WNSVGO
bovine coronavirus S	(827)	SAFWCGDYA	ACKSOLVE	YGSFCDN	INAILTE	VNELLD
mouse hepatitis virus S	(776)	AAFWCGDN	TACRQOL	VEYGSF	CVVNAIL	NEVNLL
Consensus	(841)	AAFWCGDYA	ACKSOLVE	YGSFCDN	INAILTE	VNELLD
Section 23						
	(881)	881	890	900	910	920
human coronavirus OC43 S	(857)	LQVANS	LMNGVT	LTSTKL	KDGVNF	NVDDIN
avianinfectiousbronchitisvirusS	(651)	NEYSSTKP	-----	AGENTP	VLSNV	STGEIN
bovine coronavirus S	(867)	LQVANS	LMNGVT	LTSTKL	KDGVNF	NVDDIN
mouse hepatitis virus S	(816)	LQVASA	LMOGVT	LTSSRL	PDGTS	GPIDDT
Consensus	(881)	LQVASS	LMNGVT	LTSTKL	KDGVNF	NVDDIN
Section 24						
	(921)	921	930	940	950	960
human coronavirus OC43 S	(897)	CSKASS	-----	RSATDL	LFDK	KLSDV
avianinfectiousbronchitisvirusS	(686)	SRPKRS	-----	LTEDLL	FTSV	ESVGP
bovine coronavirus S	(907)	CNKVSS	-----	RSATDL	LFDK	KLSDV
mouse hepatitis virus S	(856)	CAEDGNG	PSAIRGR	SAIEDLL	LFDK	KLSDV
Consensus	(921)	CAKSS	-----	RSATDL	LFDK	KLSDV

**FIGURE 4F (contd.)**

Section 25					
	(961)	961	970	980	990 1000
human coronavirus OC43 S	(930)	GGAE	--IRDLICVQSYKGIKVTLPPL	SENQISGYTLAATS	
avianinfectiousbronchitisvirusS	(717)	ACPLGFEKDLACAREYNGLMLPPL	ITAEQALYTSSLVA		
bovine coronavirus S	(940)	GAAE	--IRDLICVQSYNGIKVLPPL	SENQISGYTLAATS	
mouse hepatitis virus S	(896)	GGQE	--VRDLICVQSENGIKVLPPL	SESOISGYTTGATA	
Consensus	(961)	GGAE	IRDLICVQSYNGIKVLPPL	SENQISGYTLAATA	
Section 26					
	(1001)	1001	1010	1020	1030 1040
human coronavirus OC43 S	(968)	ASLPPRWTAAGV	PYYLNQYRI	NGLGVM	MDVLSQNKLI
avianinfectiousbronchitisvirusS	(757)	SMAEGGITAAGAT	PEATQDARI	PHLGH	IOSILLNDEKLI
bovine coronavirus S	(978)	ASLPPWSAAGV	PYYLNQYRI	NGHGV	TMDVLSQNKLI
mouse hepatitis virus S	(934)	AAMPPWSAAGV	PESHVQYRI	NGLGVM	IMNVLSENQKLI
Consensus	(1001)	ASLFPWSAAGV	PYYLNQYRI	NGLGVTMDVLSQ	NQKLI
Section 27					
	(1041)	1041	1050	1060	1070 1080
human coronavirus OC43 S	(1008)	NATNNLYATLE	DATNSALVK	DAV	NANAEALNNLL
avianinfectiousbronchitisvirusS	(797)	NATNNKATGHMOEG	ERSLSLQDQ	DMVSK	OSAILTETM
bovine coronavirus S	(1018)	ANATNNALGATQEG	DATNSALVK	DAV	NANAEALNNLL
mouse hepatitis virus S	(974)	NATNNALGATQD	EDATNSALGK	IOSV	NANAEALNNLL
Consensus	(1041)	ANAFNNALGATQEG	FDATNSALVK	IQAVVNANAEAL	NLL
Section 28					
	(1081)	1081	1090	1100	1110 1120
human coronavirus OC43 S	(1048)	QQLSNRFGAISASL	QEILSR	LDAL	EANAQIDRLINGRLTA
avianinfectiousbronchitisvirusS	(837)	ASENKNFGAISV	IQEYQDF	ATQNAQ	VDRLITGRSS
bovine coronavirus S	(1058)	QQLSNRFGAISSE	CEILSR	LDAL	EANAQIDRLINGRLTA
mouse hepatitis virus S	(1014)	NQLSNRFGAISASL	QEILSR	LEAVE	EAKACIDRLINGRLTA
Consensus	(1081)	QQLSNRFGAISASL	QEILSR	LDAL	EANAQIDRLINGRLTA
Section 29					
	(1121)	1121	1130	1140	1150 1160
human coronavirus OC43 S	(1088)	LNAYVSQQLSDSTLV	KESAAQAME	KVNECVK	QSRRINFC
avianinfectiousbronchitisvirusS	(877)	LSVLA	SAQAEYIRVS	QOREL	ATQRI
bovine coronavirus S	(1098)	LNAYVSQQLSDSTLV	KESAAQAME	KVNECVK	QSRRINFC
mouse hepatitis virus S	(1054)	LNAYVSQQLSDSTLV	KESAAQAME	KVNECVK	QSRRINFC
Consensus	(1121)	LNAYVSQQLSDSTLV	KESAAQAME	KVNECVK	QSRRINFC
Section 30					
	(1161)	1161	1170	1180	1190 1200
human coronavirus OC43 S	(1128)	GNGNHIISLVQNA	PYGLYFIH	FSYVPT	SFVTAKVSPGLCI
avianinfectiousbronchitisvirusS	(917)	GNGRHVLTIPONA	NGEVFIH	FSMT	DSBNVNTAIVEEGLV
bovine coronavirus S	(1138)	GNGNHIISLVQNA	PYGLYFIH	FSYVPT	SFVTAKVSPGLCI
mouse hepatitis virus S	(1094)	GNGNHIISLVQNA	PYGLYFIH	FSYVPT	SFVTAKVSPGLCI
Consensus	(1161)	GNGNHIISLVQNA	PYGLYFIH	FSYVPT	SFVTAKVSPGLCI

**FIGURE 4F (contd.)**

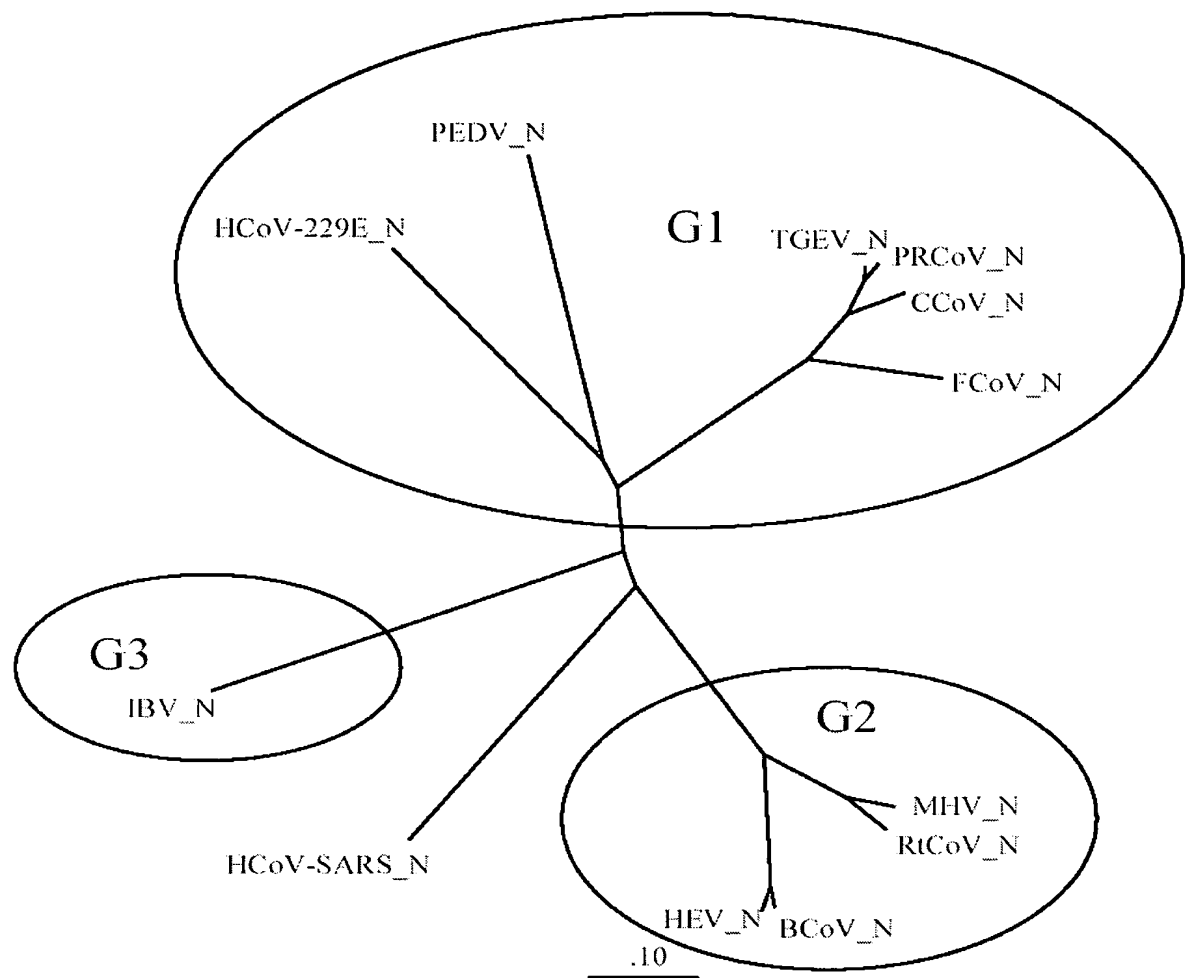
						Section 31
	(1201)	1201	1210	1220	1230	1240
human coronavirus OC43 S (1168)	AGDRG	-----	IAPKSGYFVN	VNNTWMYIGSGY	YEP	IT
avianinfectiousbronchitisvirusS (957)	KPANASQYAIVPANGROIFT	OVNGSMYI	TARDM	MPRAIT		
bovine coronavirus S (1178)	AGDRG	-----	IAPKSGYFVN	VNNTWMFTGSGY	YEP	IT
mouse hepatitis virus S (1134)	SGDRG	-----	GAAPKAGYFVQDDGEWKE	FTGSSYY	YEP	IT
Consensus (1201)	AGDRG		IAPKSGYFVN	VNNTWMFTGSGY	YEP	IT
						Section 32
	(1241)	1241	1250	1260	1270	1280
human coronavirus OC43 S (1202)	ENNVVVMSTCAVNYTKAP	VMLNTSIP	NLPD	KEELDQW		
avianinfectiousbronchitisvirusS (997)	AGDVMTITSTQANYVSVNKT	VTTFMDNDDDFD	NDELSKW			
bovine coronavirus S (1212)	GNNVVVMSTCAVNYTKAP	DVMLNISTP	NLPY	KEELDQW		
mouse hepatitis virus S (1168)	DNNSVIMSSCAVNYTKAP	EVFLNTSIP	NPPD	KEELDRW		
Consensus (1241)	ENNVVVMSSCAVNYTKAP	DVMLNTSIP	NLPD	KEELDQW		
						Section 33
	(1281)	1281	1290	1300	1310	1320
human coronavirus OC43 S (1241)	EKNQTSVAPDLSLDY	--	INVTFLDLQV	EMNLQDA	KVLN	
avianinfectiousbronchitisvirusS (1037)	WNDTKHELEDFDKEN	--	YTVPIELIDSE	EDPEKGV	TOGIN	
bovine coronavirus S (1251)	EKNQTSVAPDLSLDY	--	INVTFLDLQV	EMNLQDA	KVLN	
mouse hepatitis virus S (1207)	EKNQTSVAPDLSLDY		INVTFLDLQV	EMNLQDA	KVLN	
Consensus (1281)	EKNQTSVAPDLSLDY		INVTFLDLQV	EMNLQDA	KVLN	
						Section 34
	(1321)	1321	1330	1340	1350	1360
human coronavirus OC43 S (1279)	QSYINLKDIGTYEYV	VWKPWYVWLLIGLAGVAM	LVL	FFI		
avianinfectiousbronchitisvirusS (1075)	QSYINLKDIGTYEYV	VWKPWYVWLLIGLAGVAM	LVL	FFI		
bovine coronavirus S (1289)	QSYINLKDIGTYEYV	VWKPWYVWLLIGLAGVAM	LVL	FFI		
mouse hepatitis virus S (1247)	QSYINLKDIGTYEYV	VWKPWYVWLLIGLAGVAM	LVL	FFI		
Consensus (1321)	QSYINLKDIGTYEYV	VWKPWYVWLLIGLAGVAM	LVL	FFI		
						Section 35
	(1361)	1361	1370	1380	1390	1400
human coronavirus OC43 S (1319)	CCCTGCG	-----	TSCFKKCGGCCDDYTGHQELVIKT			
avianinfectiousbronchitisvirusS (1115)	FFMTGCGCGCCGCG	FGIMPLMS	UCKKSGYETTFDNDV	YTE		
bovine coronavirus S (1329)	CCCTGCG	-----	TSCFKKCGGCCDDYTGHQELVIKT			
mouse hepatitis virus S (1287)	CCCTGCG	-----	TSCFKKCGGCCDDYTGHQELVIKT			
Consensus (1361)	CCCTGCG		TSCFKKCGGCCDDYTGHQELVIKT			
						Section 36
	(1401)	1401	1408			
human coronavirus OC43 S (1350)	SHDD	----	SEQ ID NO: 9918			
avianinfectiousbronchitisvirusS (1155)	QYRPKKS	V	SEQ ID NO: 9909			
bovine coronavirus S (1360)	SHED	----	SEQ ID NO: 9891			
mouse hepatitis virus S (1318)	NISSHED	-	SEQ ID NO: 9902			
Consensus (1401)	SHDD					

**FIGURE 5**

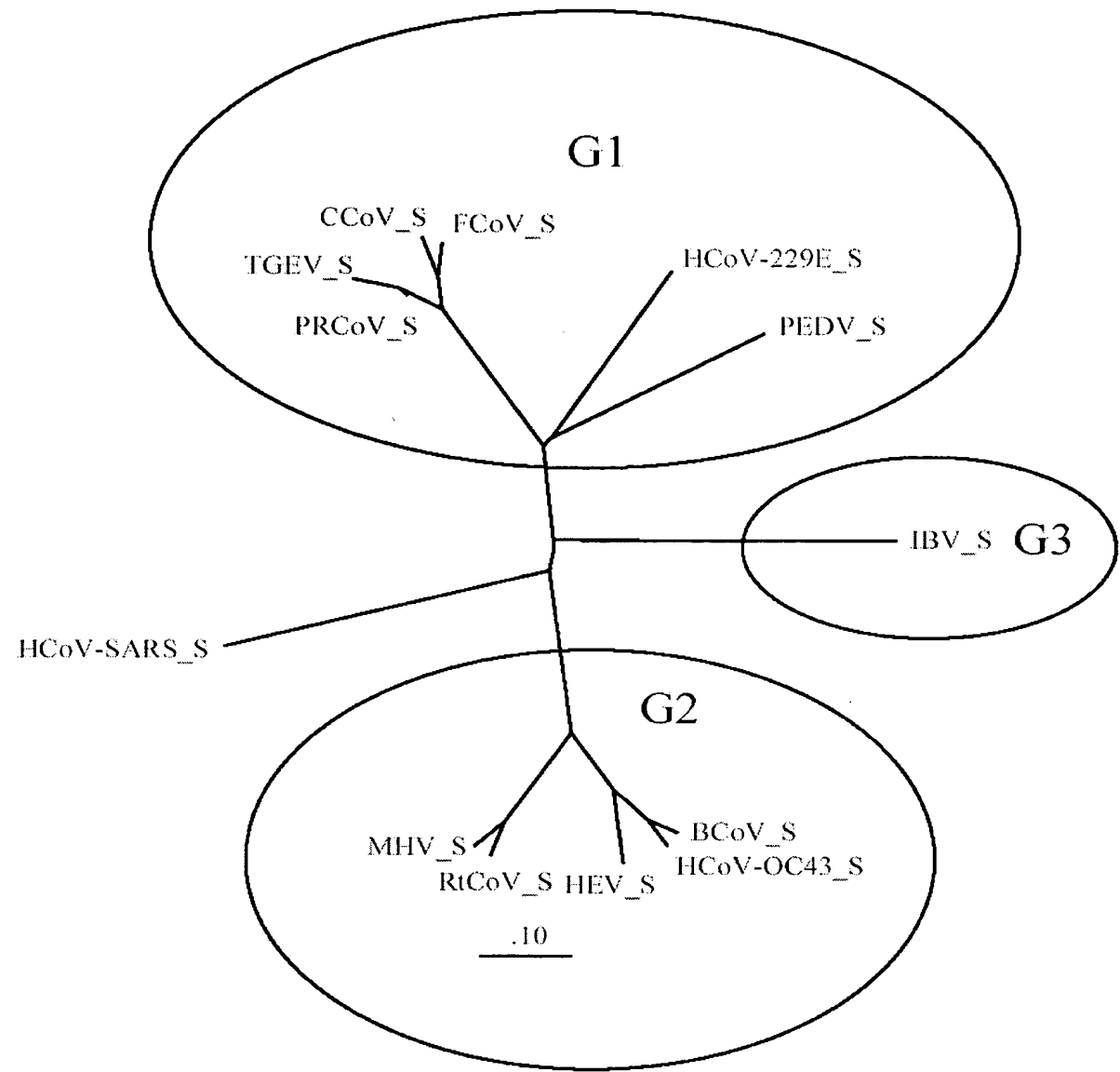
Section 15					
	(589)	589	600	610	620 630
human coronavirus OC43 S	(565)	NS	ETORPQAFLLGW	ADSC	LOGDKCNIFANFILHDVNSGLTCS
bovine coronavirus S	(575)	NPCTCQ	PQAFLLGW	EVDSCL	QGGRCNIFANFILHDVNSGTTCS
mouse hepatitis virus A59 S	(524)	KGTICANN	STLGGW	HTITGLVNDRC	QIFANFILNGLNSGTTCS
Consensus	(589)	N	CTC PQAFLLGWS	DSC	LQGGRCNIFANFILHDVNSGTTCS
Section 16					
	(631)	631	640	650	660 672
human coronavirus OC43 S	(607)	TDLQKANTD	IILGVCVNYD	LYGITG	QGIFVEVNATYYNSWQN
bovine coronavirus S	(617)	TDLQKSN	TDIILGVCVNYD	LYGITG	QGIFVEVNATYYNSWQN
mouse hepatitis virus A59 S	(566)	TDLQLENT	EMVYTC	ITV	KYDLYGCTITGGVIKEYKADYYNSWQT
Consensus	(631)	TDLQKANTD	IILGVCVNYD	LYGITG	QGIFVEVNATYYNSWQN
Section 17					
	(673)	673	680	690	700 714
human coronavirus OC43 S	(649)	LLYDSNGN	LYGFRDYITN	RTFMIR	SCYSGRVSAAFHANSSEP
bovine coronavirus S	(659)	LLYDSNGN	LYGFRDYITN	RTFMIR	SCYSGRVSAAFHANSSEP
mouse hepatitis virus A59 S	(608)	LLYDSNGN	LYGFRDYITN	RTFMIR	SCYSGRVSAAFHANSSEP
Consensus	(673)	LLYDSNGN	LYGFRDYITN	RTFMIR	SCYSGRVSAAFHANSSEP
Section 18					
	(715)	715	720	730	740 756
human coronavirus OC43 S	(691)	ALLFRNIK	CNYVFNN	SLSRQL	QPINYFDSYLGCVVNADNSTA
bovine coronavirus S	(701)	ALLFRNIK	CNYVFNN	SLSRQL	QPINYFDSYLGCVVNADNSTA
mouse hepatitis virus A59 S	(650)	ALLFRNIK	CNYVFNN	SLSRQL	QPINYFDSYLGCVVNADNSTA
Consensus	(715)	ALLFRNIK	CNYVFNN	SLSRQL	QPINYFDSYLGCVVNADNSTA
Section 19					
	(757)	757	770	780	798
human coronavirus OC43 S	(733)	ISVQTCD	LTVGSGYCV	DYSKRR	RSRRTTGYRFTNFEPFTV
bovine coronavirus S	(743)	SVVQTCD	LTVGSGYCV	DYSKRR	RSRRTTGYRFTNFEPFTV
mouse hepatitis virus A59 S	(692)	EALPNQD	PTVMGAGL	GVDDY	SKSRAHRSVSTGRLTTEDEYTP
Consensus	(757)	AVQTC	DLTVGSGYCV	DYSKRR	RSRRTTGYRFTNFEPFTV
Section 20					
	(799)	799	810	820	830 840
human coronavirus OC43 S	(775)	NSVND	SLEPVGG	LYEIQIP	SEFTTIGNMEEFIQTSSPKVTIDC
bovine coronavirus S	(785)	NSVND	SLEPVGG	LYEIQIP	SEFTTIGNMEEFIQTSSPKVTIDC
mouse hepatitis virus A59 S	(734)	MLVND	SVQSGV	DCGIFTEM	QITNEATCHHEATGTRSEKVTIDC
Consensus	(799)	NSVND	SLEPVGG	LYEIQIP	SEFTTIGNMEEFIQTSSPKVTIDC
Section 21					
	(841)	841	850	860	870 882
human coronavirus OC43 S	(817)	AAFVCGD	YAACKSQL	VEYGSF	CDNINAILTEVNELLDTTQLO
bovine coronavirus S	(827)	SAFVCGD	YAACKSQL	VEYGSF	CDNINAILTEVNELLDTTQLO
mouse hepatitis virus A59 S	(776)	AAFVCGD	YAACKSQL	VEYGSF	CDNINAILTEVNELLDTTQLO
Consensus	(841)	AAFVCGD	YAACKSQL	VEYGSF	CDNINAILTEVNELLDTTQLO

**FIGURE 6**

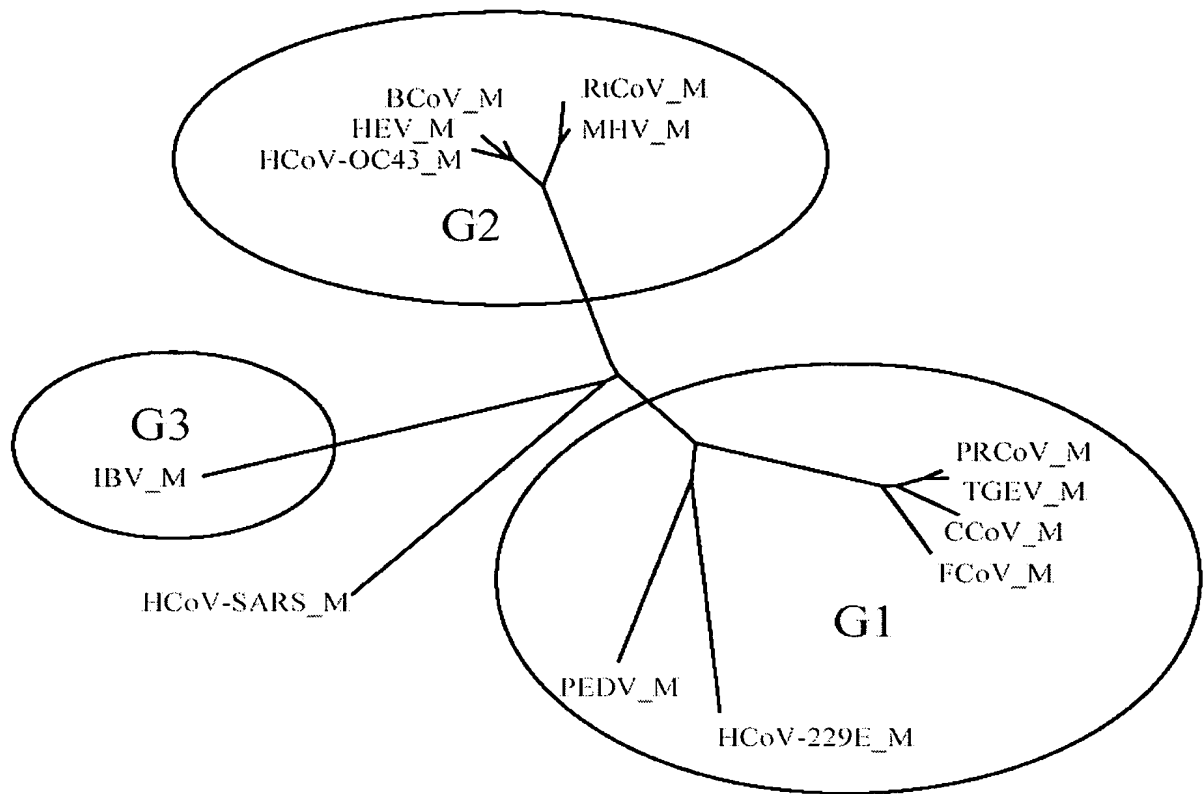
**FIGURE 6A**



**FIGURE 6B**





**FIGURE 6C**

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**FIGURE 7****FIGURE 7A**

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SEQ ID NO:6053 -----MFVLLVAYALLH----- 12
SEQ ID NO:6057 ---MKKLFVVLVVMPLIYGDNFPCSKLTNRTIGNQWNLIETFLLNYSSRLPPNSDVVLGD 60
SEQ ID NO:6061 ---MRSLIYFWLLLPLVPTLSLPQDVTRCQSTTNFRFFSKFN-----VQAPAVVVLGG 52
SEQ ID NO:6065 -----MFLILLISLPTAFAVIGDLKCTTVS-INDVDTGVPSIS----- 38
SEQ ID NO:6069 -----MLFVFILFLPSCLG YIGDFRCIQLVNSNGANVSAPSIS----- 40
SEQ ID NO:6042 -----MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRG----- 39
SEQ ID NO:6072 -----MLVTPLLLVTLCLALCSAVLYDSSS----- 27

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SEQ ID NO:6053 ----- 120
SEQ ID NO:6057 YFPTVQPWFNCIRNDSNDLYVTLENLKALYWDYATENITWNHRQRLNVVNGYPYSITVT 120
SEQ ID NO:6061 YLPSMNSSSWYCGTGIETASGVHGI FLSYIDSGQGFEIGISQEP-----FDPGGYQLYLH 107
SEQ ID NO:6065 -----TDTVDVTNGLGTY YVLD RYVLTNLTLLNG-----YY 69
SEQ ID NO:6069 -----TETVEVSQGLGTY YVLD RYVLTNLTLLTG-----YY 71
SEQ ID NO:6042 -----VYYPDEIFRSDTLYLTQDLFLPFYSNVTGFHTINHTFG-----NP 79
SEQ ID NO:6072 -----YVYYYQSAFRPPSGWHLQG----- 46

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SEQ ID NO:6053 -----IAGCQTTN-----GLNTSYSVCNG----- 31
SEQ ID NO:6057 TTRNFNSAEGAI ICICKGSPPTTTTESSLTCNWGSECLNHNKFPICPSNSEANCGNMLYG 180
SEQ ID NO:6061 KATNGNTNAIARLRICQFPDNKTLGPTVNDVTTGRNCLFNKAI PAYMRDGDIVVGITWD 167
SEQ ID NO:6065 PTSGSTYRNMALKTLLSTLWFKPPFLSDFTNGIFAKVKNTKVIKDGVMYSEFPAITIG 129
SEQ ID NO:6069 PVDGSKFRNLALTGTNSVLSWFQPPYLSQFNDGIFAKVQNLKTSTPSGATAYFPTIVIG 131
SEQ ID NO:6042 VIPFKDGIYFAATEKSNVVRGWVFGSTMNKKSQSVIIINNSTNVVIRACNFELCDNPFFA 139
SEQ ID NO:6072 -----GAYAVVNISSEFNAGSSSGCTVGIIHGGRVNVNASSIAMTAP----- 88

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SEQ ID NO:6053 ----- 240
SEQ ID NO:6057 LQWFADEVVAYLHGAS YRISFENQWSGTVTFGDMRATTLVAGTLVDLWVFNVPYDVSY 240
SEQ ID NO:6061 -----NDRVTVFADKIYHFYLNKNDWSRVATRCYNRRSCAMQYVYPTPYMLN----- 214
SEQ ID NO:6065 -----STFVNTSYSVVQPHTTILGNKLGQFLEISVCQYTMCEYPNT 171
SEQ ID NO:6069 -----SLFGYTSYTVVIEPYN-----GVIMASVCQYTICLLPYT 165
SEQ ID NO:6042 VS-----KPMGTQHTMI FDNAFN----- 158
SEQ ID NO:6072 -----

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SEQ ID NO:6053 -----CVGYSENVFAVESGGYIPSDFAFNNWFLLTNTSSVVDGVVRSF 74
SEQ ID NO:6057 RVNNKNGTTVVSNCTDQCASYVANVFTTQPGGFIPSDFSFNNWFLLTNSSTLVSGKLVT 300
SEQ ID NO:6061 VTSAGEDGIYYEPTANCTGYAANVFATDSNGHIPEGFSFNNWFLLSNDSTLLHGKVSN 274
SEQ ID NO:6065 ICNPN-LGNQRVELWHWDTG VVSCLYKRNFYTDVNADYLYFHFYQEGGT FYAYFTDTGVV 230
SEQ ID NO:6069 DCKPNTNGNKLIGFWHTDVKPPICVLKRNF TLNVNADAFYFHFYQHGGTFYAYYADKPSA 225
SEQ ID NO:6042 -CTFEYISDAFSLDVSEKSGNFKHLREFVFNKDGFLYVYKGYQPIDVVRDLPSGFNTLK 217
SEQ ID NO:6072 -----SSGMAWSSSQFCTAHCNFSDDTVFVTHCYKHGG--CPLTGMLQQN 131

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SEQ ID NO:6053 QPLLLNCLWSVSGLRFTTG FVYFNGTGRGDCKGFSSDVLSDVIRYNLNFEENLRG---T 131
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SEQ ID NO:6061 QPLLVNCLLAIPKIYGLGQFFSFNHTMDGVCNGAAVDRAPEALRFNINDTSVILAEG--S 332
SEQ ID NO:6065 TKFLFNVLGTVL SHYYVMPLTCN----SALTLEYWVTP LTKQYLLAFNQDGVIFNAVD 286
SEQ ID NO:6069 TTFLFSVYIGDILTQYYVLPFICNPTAGSTFAPRYWVTP LVKRQYLFNFNQKVITSADV 285
SEQ ID NO:6042 PIFKPLGINITNFRAILTAFSPAQDIWGTSAAYFVG YLKPTTFMLKYDENGITDAVD 277

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SEQ ID NO: 6072 LIRVSAMKNGQLFYNLTVSVAKYPTFRSFQCVNNLTSVYLNGLDLYTSNETIDVTSAGVY 191  
  
 SEQ ID NO: 6053 ILFKTSYG---VVVFYCTNNT-LVSGDAHIPFGTVLGNFYCFVNTTIGNETTSFVFGAL 186  
 SEQ ID NO: 6057 VFSLNTTGGVTLEISCYTVSDS-SFFSYGEIPFGVTDGPRYCYVHY---NGTALKYLGTL 416  
 SEQ ID NO: 6061 IVLHTALG---TNLSFVCSNSSDPHLAIFAIPLGATEVPYYCFLKVDYNTSVYKFLAVL 389  
 SEQ ID NO: 6065 CKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVRRIPNLPDCN-IEAWLNDKSVPS 345  
 SEQ ID NO: 6069 CASSYTSEIKCKTQSMPLSTGVYELSGYTVQPVGVVYRRVANLPACN-IEEWLTARSVPS 344  
**SEQ ID NO: 6042 CSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPGDVVR-FPNITNLCPFGEVFNATKFPS 336**  
 SEQ ID NO: 6072 FKAGGPITYKVMREVKALAYFVNGTAQDVLICDGSPRGLLACQYNTGNFSDGFYPTNSS 251  
  
 SEQ ID NO: 6053 PKTVREFVISRTGHFYINGYRYFTLGNVEAVNFNVT----TAETTDFACTVALASYADVLV 242  
 SEQ ID NO: 6057 PPSVKEIAISKWGHFYINGYNFFSTFPIDCISFNLT----TGSDVFWTIAYTSYTEALV 472  
 SEQ ID NO: 6061 PPTVREIVITKYGDVYVNGFGYHLGLLDAVTINFTGHGTDDDVSGFWTIASNFVDALI 449  
 SEQ ID NO: 6065 PLNWERKTFSNCFNMSSLSFIQAYSFTCNNIDAA----KIYGMCFSSITIDKFAIPNG 401  
 SEQ ID NO: 6069 PLNWERKTFQNCNFNLSLLRYVQAESLFCNNIDAS----KVYGRCFGSSISVDKFAVPRS 400  
**SEQ ID NO: 6042 VYAWERKKISNCVADYSVLNSTFFSTFKCYGVSAT----KLNDLCFSNVYADSFVVKGD 392**  
 SEQ ID NO: 6072 LVKQKFIVYRENSVNTTCTLHNFIHNETGANPNPSG--VQNIQTYQTKTAQSGYYNFNF 309  
  
 SEQ ID NO: 6053 NVSQTSIANIYCNVINRLRCDQLSFDVPDGFYSTSP--IQSVELPVSIVSLPVYHKHT 300  
 SEQ ID NO: 6057 QVENTAITKVITYCNHVNNIKSCQITANLNGFYVPSS--SEVGLVNKSVVLLPSFYTHT 530  
 SEQ ID NO: 6061 EVQGTSIQRILYCDPVSQKCSQVAFDLDDGFYPISSRNLLSHEQPISEFVTLPSFNDHS 509  
 SEQ ID NO: 6065 RKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAAVNS--VSRFPSTWNRFRGFTEQS 459  
 SEQ ID NO: 6069 RQVDLQLGNSGFLQTANYKIDTAATSCQLHYTLPKNNVT--INNHNPSWNRRYGFENDAG 458  
**SEQ ID NO: 6042 DVRQIAPGQTGVADIADYNYKLPPDFMGCVLAWNTRNIDAT-----STGNINYKYRILRHG 446**  
 SEQ ID NO: 6072 SFLSSFVYKESNFMYGSYHPSCKFRLETINGLWFNSLS-----VSIAYGPLQGCKQS 363  
  
 SEQ ID NO: 6053 FIVLYVDFKPQ-SGGGKCFNCYPAGVNITLANFNET---KGPLCVDTSHTTKYVAVYAN 356  
 SEQ ID NO: 6057 IVNITIGLGMKRSYGQPIASTLS--NITLPMQDHN---TDVYCIRSDQFS-VYVHSTCK 584  
 SEQ ID NO: 6061 FVNITVS-----AAFGLSSANLVASDTTNGFSS-----FCVDTRQFTITLIFYNVTN 557  
 SEQ ID NO: 6065 VFKEPQAGVFTDHDVVYAQHCFAKSTNFCPCCKLDGSLCVGNGPGIDAGYKTSIGTCPCAG 519  
 SEQ ID NO: 6069 VFGKN-----QHDVVYAQQCFTRSSYPCP----- 483  
**SEQ ID NO: 6042 KLRPFER----- 453**  
 SEQ ID NO: 6072 VFKEGRAT----- 370  
  
 SEQ ID NO: 6053 VGRWS-----ASINTGNCPFSFGKVNNFVKFGSVCFSCLKDIPGGCAMPIVA 402  
 SEQ ID NO: 6057 SALWDNIFKRNCTDVLDAVIAIKTGTCPFSFDKLNLYLTFNKFCLSLSPVGANCKFDVAA 644  
 SEQ ID NO: 6061 SYGYVS-----KSQDSNCPFTLQSVNDYLSFSKFCVSTSLLAGACTIDLFG 603  
 SEQ ID NO: 6065 TNYLTCHNAAQCDCCLCTPDPITSKATGPYKCPQTKYLVGIGEHCSGLAIKSDHCG---G 575  
 SEQ ID NO: 6069 -----AQPDI VSPCTT---QTKPKSAFVNVDHCEGLGVLEDNCGNADPH 525  
**SEQ ID NO: 6042 -----DISNVFFSPDGKPCPTPPALNCYWLND 480**  
 SEQ ID NO: 6072 -----CCYAYSYGGPSLCKGVYSGELDHNFECEGL 399  
  
 SEQ ID NO: 6053 NWAYSKY---YTIG-----SLYVSWSDGDGITGVPQVEGVSSFMNVTLDKC 446  
 SEQ ID NO: 6057 -RTRTNE---QVVR-----SLYVIYEEDNIVGVPSDNGSVHDLVSLHLDSC 687  
 SEQ ID NO: 6061 YPAFGSG---VKLT-----SLYFQFTKGELITGTPKPLEGITDVSFMTLDVC 647  
 SEQ ID NO: 6065 NPCTCQP---QAFLGWSVSDCLQGDRCNIFANFILHDVNSGTTCTDLQKSNTDIILGVC 632  
 SEQ ID NO: 6069 KGCICAN---NSFIGWSHDTCLVNDRCQIFANILLNGINSGTTCTDLQLPNTVEVVTGIC 582  
**SEQ ID NO: 6042 YGFYTTTGIGY-----QPYRVVLSFELLNAPATVCGPKLSTDLIKNQ 524**  
 SEQ ID NO: 6072 LVYVTKS-----GGSRIQTATEPPVITQNNYNNITLNTC 433

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SEQ ID NO:6053   TKYNIYDVSGVGVIIRVSNDFLN-----GITYTSTSGNLLGFKDKVTIYSITPC 497
SEQ ID NO:6057   TDYNIYGRGTGVGIIRQTNRTLLS-----GLYYTSLSGDLLGFKNVSDGVIYSVTPC 738
SEQ ID NO:6061   TKYTIYGFKGEGIIITLTNSSILA-----GVYYTSDSGQLLAFKNVTS GAVYSVTPC 698
SEQ ID NO:6065   VNYDLYGITQGQIFVEVNATYYNS-----WQNLLYDSNGNLGYFRDYLTNRFTMIRSC 685
SEQ ID NO:6069   VKYDLYGITQGQVFKEVKADYYNS-----WQTLLYDVNGNLNGFRDLTTNKTYTIRSC 635
SEQ ID NO:6042   VNFNFNGLTGTGVLTPSSKRFP-----FQQFGRDVSDFTDSDVRDPKTSEILDISP 576
SEQ ID NO:6072   VDYNIYGRGTGGFITNVTD SAVSYNYLADAGLAILD TSGSIDIFVVQGEYGLNYYKVNPC 493
      . : . * * : . . . : . *

SEQ ID NO:6053   NPPDQLVVYQQA--VVGAMLS ENFTSYGFSNVVELPKFFYASNGTYN----- 542
SEQ ID NO:6057   DVSAQA AVIDGT--IVGAITSINSELLGLTHWTTTPNFYYYSIYNTND RTRGTAIDSND 796
SEQ ID NO:6061   SFSEQAAYVND--IVGVISLSNS--TFNNRELPGFFYHSNDGSN----- 741
SEQ ID NO:6065   YSGRVSA AFHAN--SSEPALLFRNIKCN YFNNTLSRQLQPINYFDSYLGC VVNADNSTS 743
SEQ ID NO:6069   YSGRVSA AFHKD--APEPALLYRNINC SYVFSNNISREENPLNYFDSYLGC VVNADNRD 693
SEQ ID NO:6042   AFGGVSVITPGTNASSEVA VL YQDVNCTDVSTAIHADQLTPAWRIYSTGN NV FQTQAGCL 636
SEQ ID NO:6072   EDVNQQFVVS GGK-LVGILT SRNETGS QLENQFYIKITNGTRRFRRSITEN----- 544

SEQ ID NO:6053   -CTDAVLTYSSFGVCADGS-----IIAVQPRNVSYDSVSAIVTAN-----LSI 584
SEQ ID NO:6057   VDCEPVITYSNIGVCKNGA-----FVFINVTHSDGD-VQPISTGN-----VTI 838
SEQ ID NO:6061   -CTEPVLVYSNIGVCKSGS-----IGYVPSQYQVK-IAPT VTGN-----ISI 782
SEQ ID NO:6065   SVVQTCDLTVGSGYCVDYSTKRRSR SITTG YRFTNFEPFTVNS VND SLEPVGGLYEIQI 803
SEQ ID NO:6069   EALPNCDLRMGAGLCVDYSGKSRRADR SVSTGYRLTTFEPT PMLVND SVQSVDGLYEMQI 753
SEQ ID NO:6042   I GAEHVDTSYECDIP IGACISYHTVSLSTRSQKSIVAYTMSLGADSSIAYS NN TIAI 696
SEQ ID NO:6072   VANCPYVS YGKF CIKPDGS-----IATIVPKQLEQFVAPLFNV TEN-----VLI 588
      . . : *

SEQ ID NO:6053   PSNWTTSVQVEYLQITSTPIVDCSTYVCNGNVRCVELLKQYTSACKTIEDALRNSARLE 644
SEQ ID NO:6057   PTNFTISVQVEYIQVYTTPV SIDCSRYVCNGNPRCNKLLTQYVS ACQTIEQALAMGARLE 898
SEQ ID NO:6061   PTNFSMSIRTEY LQLYNTPVSVDCATYVCNGNSRCKQLLTQYTAACKTIESALQL SARLE 842
SEQ ID NO:6065   PSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAA CKSQLVEYGSFCDNINA ILTEVNELL 863
SEQ ID NO:6069   PTNFTIGHHEEFIQTRS PKVTIDCAAFVCGDNTACRQQLVEYGSFCVNVNAILNEVNNLL 813
SEQ ID NO:6042   PTNFSISITTEVPVSM AKTSVDCNM YICGDSTECANLLLQYGSFCTQLNRALS GIAAEQ 756
SEQ ID NO:6072   PNSFNLTVTDEY IQTRMDKVQINCLQYVCGSSLDCRKLFQQYPVCDNILSVVNSV GQKE 648
      *... * : ::* :*:.. * . : :* . * : :

SEQ ID NO:6053   SADVSEMLTFDKKAFTLANVSSFGDYN-----LSSVIPSLPTSGS---- 684
SEQ ID NO:6057   NMEVD SMLFVSENALKLASVEAFNSSETLDPIYKEWP NIGGSWLEGLKYILPSHNS---- 954
SEQ ID NO:6061   SVEVNSMLTISEEALQLATISSFNGDG-----YNFTNV LGASVYDPASGR---- 887
SEQ ID NO:6065   DTTQLQVANSLMNGVTLSTKLKDGVNFN-----VDDINFSPVLGCLGSDCN---- 909
SEQ ID NO:6069   DNMQLOVASALMQGVTISSRLPDGISGP-----IDDINFSP LLGCIGSTCAEDGN 863
SEQ ID NO:6042   DRNTREVFAQVKQMYKTPTLKYFGGFN-----FSQILPDPLKPTK---- 796
SEQ ID NO:6072   DMELLN FY SSTKPAGFNPVLSNVSTG-----EFNISLLLTNPSSRRK---- 691
      . . .

SEQ ID NO:6053   ---RVAGRSAIEDILFSKLVTSGLGTVDADYKKCTKGLS--IADLACAQYYNGIMVLP GV 739
SEQ ID NO:6057   ---KRKYRSAIEDLLFDKVVT SGLGTVDEDYKRCTGGYD--IADLVCAQYYNGIMVLP GV 1009
SEQ ID NO:6061   ---VVQKRSVIEDLLFNKVVTNGLGTVDEDYKRCSNGRS--VADLVCAQYYSGVMVLP GV 942
SEQ ID NO:6065   ---KVSSRSAIEDLLFSKV KLSDVG-FVEAYNNCTGGAE--IRD LICVQSYNGIKVLP PL 963
SEQ ID NO:6069   GPSAIRGRSAIEDLLFDKV KLSDVG-FVEAYNNCTGGQE--VRD LLCVQSFNGIKVLP PV 920
SEQ ID NO:6042   -----RSFIEDLLFNKVTLADAG-FMKQYGECLGDIN--ARDLICAQKFNGLT VLPPL 846
SEQ ID NO:6072   -----RS LIEDLLFTSVESVGLP-TNDAYKNCTAGPLGFFKDLACAREYNLLVLPPI 743
      ** ****.* * * * *

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SEQ ID NO: 6053 ADAERMAMYTGSLIGGIALGGLTS----AVSIPFSLAIQARLNYVALQTDVLQENQKILA 795  
 SEQ ID NO: 6057 ANADKMTMYTASLAGGITLALGGG---AVAIPFAVAVQARLNYVALQTDVLNKNQKILA 1066  
 SEQ ID NO: 6061 VDAEKLHMYASLIGGMALGGITA----AALPFSYAVQARLNYLALQTDVLQRNQQLLA 998  
 SEQ ID NO: 6065 LSENQISGYTLAATSASLFPPWSA----AAGVPFYLNVQYRINGIGVTMDVLSQNKLIA 1019  
 SEQ ID NO: 6069 LSENQISGYTTGATAAAMFPPWSA----AAGVPFSLSVQYRINGLVTMNVLSQNKMIA 976  
**SEQ ID NO: 6042 LTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIA 906**  
 SEQ ID NO: 6072 ITAEMQALYTSSLVASMAFGGITA----AGAIPFATQLQARINHLGITQSLLLNQEKIA 799  
 . \*: . . . \* : \*\* : \* : \* : . : \* . \* : \*

SEQ ID NO: 6053 ASFNKAMTNIVDAFTGVNDAITQTSQALQTVATALNKIQDVVNQQGNSLNHLTSQLRQNF 855  
 SEQ ID NO: 6057 SAFNQAIGNITQSFGKVNDIAHQTSRGLATVAKALAKVQDVVNIQQQALSHLTVQLQNNF 1126  
 SEQ ID NO: 6061 ESFNSAIGNITSFAESVKEAISQTSKGLNTVAHALTKVQEVVNSQGSALNQTLTVQLQHNF 1058  
 SEQ ID NO: 6065 NAFNNALGAIQEGFDATN-----SALVKIQAVVNANAEALNNLLQQLSNRF 1065  
 SEQ ID NO: 6069 SAFNNALGAIQDGFATN-----SALGKIQSVVNANAEALNNLLQQLSNRF 1022  
**SEQ ID NO: 6042 NQFNKAISQIQESLTTTS-----TALGKLQDVVNQNAQALNTLVKQLSSNF 952**  
 SEQ ID NO: 6072 ASFNKAIGHMQEGFRSTS-----LALQQIQDVVSKQSAILTETMASLNKNF 845  
 \*\*.\*: : . : . . \*\* : \* \*\* : . \* . \* . \*

SEQ ID NO: 6053 QAISSSIQAIYDRLDTIQADQQVDRLITGRLAALNVFVSHTLTKEYTEVRASRLAQQKVN 915  
 SEQ ID NO: 6057 QAISSSIDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVRASRLAKDKVN 1186  
 SEQ ID NO: 6061 QAISSSIDDIYSRLDILSADVQVDRLITGRLSALNAFVAQTLTKYTEVQASRLAQQKVN 1118  
 SEQ ID NO: 6065 GAISSSLQEILSRDALEAQAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAQAAMEKVN 1125  
 SEQ ID NO: 6069 GAISASLQEILTRLEAVEAKAQIDRLINGRLTALNAYISKQLSDSTLIKVSAAQAIKVN 1082  
**SEQ ID NO: 6042 GAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVTQQLIRAAEIRASANLAATKMS 1012**  
 SEQ ID NO: 6072 GAISSVIQEIYQQFDAIQANAQVDRLITGRLSLSVLASAKQAEYIRVSQQRELATQKIN 905  
 \*\*\*: . : \* : : . : \* . \* : \* : \* : \* : \* : : : : . : \* \* : .

SEQ ID NO: 6053 ECVKSQSKRYGFCG-NGTHIFSIVNAAPEGLVFLHTVLLPTQYKDVEAWSGLCVDG---- 970  
 SEQ ID NO: 6057 ECVRSQSQRFGFCG-NGTHLFSLANAAPNGMIFHTVLLPTAYETVTAWPGICASDG-DR 1244  
 SEQ ID NO: 6061 ECVKSQSQRYGFCGGDGEHIFSLVQAAPQGLLFLHTVLPVPGDFVNVLAIAGLCVNG---- 1174  
 SEQ ID NO: 6065 ECVKSQSSRINFCEG-NGNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAG---- 1180  
 SEQ ID NO: 6069 ECVKSQTTRINFCEG-NGNHILSLVQNAPYGLYFIHFSYVPISFTTANVSPGLCISG---- 1137  
**SEQ ID NO: 6042 ECVLGGQSKRVDFCG-KGYHLSMFPQAAPHGVFLHVTYVPSQERNFTTAPAICHEG---- 1067**  
 SEQ ID NO: 6072 ECVKSQSIRYSFCG-NGRHVLTIPQNAPEGIVFIHFSYTPDSFVNVTIAIVGFCVKPANAS 964  
 \*\*\* .\*: \* .\*\*\* . \* \* : : : : \* \* \* : \* \* \* . : \*

SEQ ID NO: 6053 TNGYVLRQPNLALYK-----EGNYRITSRIMFEPRIPTMADFVQIENCNVTFVNISRS 1024  
 SEQ ID NO: 6057 TFGLVVKDVLQTLFRN-----LDDKFYLTPTMTYQPRVATSSDFVQIEGCDVLFVNATVS 1299  
 SEQ ID NO: 6061 EIALTLREPGLVLFTHLQTYTATEYFVSSRRMFEPKPTVSDVQIESCVVTVYNLTSD 1234  
 SEQ ID NO: 6065 DRGIAPKSGYFVNVNN-----TWMFTGSGYYPPEPITGNNVVMSTCAVNYTKAPDV 1232  
 SEQ ID NO: 6069 DRGLAPKAGYFVQDDG-----EWKFTGSSYYPPEPITDKNSVIMSSCAVNYTKAPEV 1189  
**SEQ ID NO: 6042 -KAYFPREGVVFNGT-----SWFITQRNFFSPQIITDNTFVSGNCDVVGIIINNT 1118**  
 SEQ ID NO: 6072 QYAIVPANGRGIFIQVN-----GSYYITARDMYMPRAITAGDVVTLTSCQANYVSVNKT 1018  
 . : : : \* . \* : . \* .

SEQ ID NO: 6053 ELQTIVP-EYIDVNKTLQELSYKL-PNYTVPDLVVEQYNQTLNLTSEISTLENKSAELN 1082  
 SEQ ID NO: 6057 DLPSIIP-DYIDINQTVQDILENFRPNWTVPELTFDIFNATYLNLTGEIDDLERSEKLH 1358  
 SEQ ID NO: 6061 QLPDVIP-DYIDVNKTLDEILASL-PNRTGPSLPLDVFNATYLNLTGEIADLEQRSESLR 1292  
 SEQ ID NO: 6065 MLNISTP-NLPYFKEELDQWFKNQTSVAPDLSLDY--INVTFLDLQDEM----- 1279  
 SEQ ID NO: 6069 FLNTSIP-NPPDFKEELDKWFKNQTSIAPDLSLDFEKLNVTLTLLDLYEMN----- 1238  
**SEQ ID NO: 6042 VYDPLQP-ELDSFKEELDKYFKNHTSPVDLGDIG-INASVVNIQKEID----- 1166**  
 SEQ ID NO: 6072 VITTFVDNDDDFDNELSKWVNDTKHELPDFDKFN--YTVPILDIDSEID----- 1066  
 : . : . : . . . : : \* :

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SEQ ID NO:6053 YTVQKLQTLIDNINSTLVDLKWLNRVETIYKWPWWVWLCISVVLIFVVSMLLLCCCSTGC 1142
SEQ ID NO:6057 NTTVELAILIDNINNTLVNLEWLNRIETIYKWPWYVWLLIGLVVIFCIPLLLFCCCSTGC 1418
SEQ ID NO:6061 NTTEELRSLINNINNTLVLDLEWLNRVETIYKWPWWVWLIIVIVLIFVVSLLVFCCISTGC 1352
SEQ ID NO:6065 ----RLQEAIKVLNQSYINLKDIGTYEYVYKWPWYVWLLIGFAGVAMLVLLFFICCCTGC 1335
SEQ ID NO:6069 ----RIQDAIKKLNESYINLKEVGTYEMYVYKWPWYVWLLIGLAGVAVCVLLFFICCCTGC 1294
SEQ ID NO:6042 ----RLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMTTILCCMTSC 1222
SEQ ID NO:6072 ----RIQGVIQGLNDSLIDLEKLSILKTYIKWPWYVWLAIAFATIIIFILILGWVFFMTGC 1122
      .:      . :*. : :*: :. : :*.*****:*** : : : : *.*

SEQ ID NO:6053 CGFFSCFA-----SSIRGCCSTKLPYYD-VEKIHQ--- 1173
SEQ ID NO:6057 CGCIGCLG-----SCCHSICSRQFENYEPIEKVHVH--- 1450
SEQ ID NO:6061 CGCCGCCG-----ACFSGCCRGPRLPYEAFAEKVHVQ--- 1384
SEQ ID NO:6065 G--TSCFK-----KCGGCCDDYTGHQELVIKT---SHED- 1364
SEQ ID NO:6069 G--SCCFK-----KCGNCCDEYGGHQDSIVIHNISSED- 1326
SEQ ID NO:6042 CSCLKGAC-----SCG-SCCKFDEDDSEPVLGKVKLHYT- 1255
SEQ ID NO:6072 CGCCCGCFGIMPLMSKCGKSSYYTTFDNDVVTEQYRPKKS 1164

```

**FIGURE 7B**

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SEQ ID NO:6054 -----MFLKLVDHHA-LVVNVLLWCVVLIVILLVCITIIKLIKLCFTCHMFCNRTVY 51
SEQ ID NO:6062 -----MLQLVNDNG-LVVNVILWLFLVLFLLIISITFVQLVNLCTCHRLCNSAVY 54
SEQ ID NO:6058 ----MTFPRALTVIDDNG-MVINIIFWFLIIILILLSIALLNIIKLCMVCCNLGRTVII 59
SEQ ID NO:6045 -----MYSFVSEETGTLIVNSVLLFLAFVVFLLVTLAILTALRLCAYCCNIVNVSLV 52
SEQ ID NO:6073 -----MNLNKSLEENG-SFLTALYIIIVGFLALYLLGRALQAFVQAADACCLEFWYTWV 57
SEQ ID NO:6066 -----MFADAYFADTVWYVVGQIIFIVAICLLVIIVVVAFLATFKLCIQLCGMCNTLVL 54
      :      .      :      . . : : : : : :

SEQ ID NO:6054 GP----IKNVYH-IY-QSYMH-----IDPF-----PKRVIDF----- 77
SEQ ID NO:6062 TP----IGRLYR-VY-KSYMR-----IDPL-----PSTVIDV----- 80
SEQ ID NO:6058 VP----AQHAYD-AY-KNFM-----IKAYN-----PDGALLA----- 86
SEQ ID NO:6045 KP----TVYVYS-RV-KNLNS-----SEGV-----PDLLV----- 76
SEQ ID NO:6073 IPGAKGTAFVYKYTYGRKLNNPELEAVIVNEFPKNGWNNKNPANFQDAQRDKLYS 112
SEQ ID NO:6066 SP----SIYVEN-RG-RQFYEF-----YNDVKP-----PVLVDVDDV----- 84
      *      :      :.      .      *

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**FIGURE 7C**

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SEQ ID NO:6055 -----MSNDNC-----TGDIVTHLKNWNF 19
SEQ ID NO:6063 -----MSNGSIP-----VDEVIEHLRNWNF 24
SEQ ID NO:6059 ----MKILLILACVIACACGERYCAMKSDTDLSCRNSTASDCESCFCNGGDLIWHLANWNF 60
SEQ ID NO:6067 -----MSSVT-TPAPVYTWT-----ADEAIKFLKEWNF 27
SEQ ID NO:6070 -----MSSTTQAPEPVYQWT-----ADEAVQFLKEWNF 33
SEQ ID NO:6046 -----MADNGTIT-----VEELKQLLEQWNL 21
SEQ ID NO:6074 -----MPNETNCTLD-----FEQSVQLFKEYNL 28
      *      .      :      : :*:

SEQ ID NO:6055 GWNVILTFIVILQFGHYKYSRLFYGLKMLVLWLLWPLVLALSIFDTWANWDSN-WAFVA 78
SEQ ID NO:6063 TWNIILTILLVVLQYGHYKYSVFLYGVKMAILWILWPLVLALSIFDAWASFQVN-WVFFA 83
SEQ ID NO:6059 SWSIILIVFITVLQYGRPQFSWFYGIKMLIMWLLWPVVLALTIFNAYSEYQVSRYVMFG 120
SEQ ID NO:6067 SLGIILLFITVILQFGYTSRSMFVYVVKMVLWLMWPLTIILTIFN--CVYALN-NVYLG 84
SEQ ID NO:6070 SLGIILLFITIILQFGYTSRSMFIYVVKMILWLMWPLTIVLCIFN--CVYALN-NVYLG 90
SEQ ID NO:6046 VIGFLFLAWIMLLQFAYSNNRNFYIILKLVFLWLLWPVTLACFVLA--AVYRIN-WVTGG 78

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SEQ ID NO: 6074 FITAFLLFLTIILQYGYATRSKVIYTLKMIVLWCFWPLNIAVGVIS--CTYPPN-TGGLV 85  
 :: : \*\* : . . . \* : \* : \* : : : : .

SEQ ID NO: 6055 FSFFMAVSTLVMWVMYFANSFRLFRRARTFWAWNPEVNAITVTTVL-QQTYYPQIQQAAPT 137  
 SEQ ID NO: 6063 FSILMACITLMLWIMYFVNSIRLWRRTHSWWSFNPETDALLTTSVM-GRQVCIPVLGAPT 142  
 SEQ ID NO: 6059 FSIAGAIVTFVLWIMYFVRSIQLYRRTKSWSFNPETKAILCVSAL-GRSYVLPLEGVPT 179  
 SEQ ID NO: 6067 FSIVFTIVAIIMWIVYFVNSIRLFIRTGSWWSFNPETNNLMCIDMK-GRMYVRPIIEDYH 143  
 SEQ ID NO: 6070 FSIVFTIVSIVIWIMYFVNSIRLFIRTGSWWSFNPETNNLMCIDMK-GTVYVRPIIEDYH 149  
**SEQ ID NO: 6046 IAIAMACIVGLMWLSYFVASFRLFARTSRMWSFNPETNILLNVPLR-GTIVTRPLMESEL 137**  
 SEQ ID NO: 6074 AAILTVFACLSFVGWYIQSIRLEKRCRSWWSFNPESNAVGSIILLTNGQQCNFAIESVPM 145  
 : : : : \* : \* : \* : \* : \* : \* : \*

SEQ ID NO: 6055 GITVTLLSGVLYVDGHRLASGVQVHNLPEYMTVAVPSTTIISRVGRSVNSQNSTG--WV 195  
 SEQ ID NO: 6063 GVTLTLLSGTLLVEGYKVATGVQVSQLPNFVTVAKATTIVYGRVGRSVNASSGTG--WA 200  
 SEQ ID NO: 6059 GVTLTLLSGNLYAEGFKIAGGMNIDNLPKYVMVALPSRTIVYTLVGKKLKASSATG--WA 237  
 SEQ ID NO: 6067 TLTVTIIRGHLYMQGIKLTGYSLSDLPAYVTVAKVSHLLTYKRG-FLDKIGDTSG--FA 200  
 SEQ ID NO: 6070 TLTATIIRGHLYMQGVKLTGFSLSDLPAYVTVAKVSHLCTYKRA-FLDKVDGVSG--FA 206  
**SEQ ID NO: 6046 VIGAVIIRGHRLRMAGHSLGR-CDIKDLPKEITVATS-RTLSYYKLGASQVRGTDG--FA 193**  
 SEQ ID NO: 6074 VLSPIIKNGVLYCEGQWLAK-CEPDHLPKDFVCTPDRRIYRMVQKYTGQSGNKKRFA 204  
 : : \* \* \* : . . \*\* : \* . \* . :

SEQ ID NO: 6055 FYVRVKHGDFAVSSPMSNMTENERLLHFF 225  
 SEQ ID NO: 6063 FYVRSKHGDYSAVSNPSAVLTDSEKVLHLV 230  
 SEQ ID NO: 6059 YYVKSAGDYSTEAR-TDNLSEKELLMHV 266  
 SEQ ID NO: 6067 VYVKSQVGNRYRLPSTQKGSGLDTALLRNNI 230  
 SEQ ID NO: 6070 VYVKSQVGNRYRLPSN-KPSGADTALLR--I 233  
**SEQ ID NO: 6046 AYNRYRIGNYKLNTDHAGSNDNIALLVQ-- 221**  
 SEQ ID NO: 6074 TFVYAKQSVDTGELESVATGSSSLYT---- 230  
 : : . . .

**FIGURE 7D**

SEQ ID NO: 6056 -----MATVKWADASE-----PQRGRQG----- 18  
 SEQ ID NO: 6064 -----MASVSF-----QDRGRK----- 17  
 SEQ ID NO: 6060 -----MANQGQRVSWGDEST-----KTRGRSNSRGRKN----- 31  
 SEQ ID NO: 6068 MSFTPGKQSSS-RASSGNRSGNGILK---WADQSDQSRNVQTRGRR-AQPKQTATSQQPS 55  
 SEQ ID NO: 6071 MSFVPGQENAGGRSSSVNRAGNGILKTTWADQTERGPNNQNRGRR-NQPKQTATTQ-PN 58  
**SEQ ID NO: 6051 -----MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQGLPN 48**  
 SEQ ID NO: 6075 -----MASGKAAGKTDA PAPVIKLGPKP-----PKVGSS----- 35  
 . . . \*

SEQ ID NO: 6056 ----RIPYSLYSPLLVDSEQPW-KVIPRNLVPINKK-DKNKLIGYWN--VQKRFRTRKGK 70  
 SEQ ID NO: 6064 ----RVPLSLYAPLRVTNDKPLSKVLANNAVPTNKG-NKDQQIGYWN--EQIRWRMRGE 70  
 SEQ ID NO: 6060 ---NNIPLSFFNPITLQQGSKFWNLCPDFVPKGIG-NRDQQIGYWN--RQTRYRMVKGQ 85  
 SEQ ID NO: 6068 GGNVVPYYSWFSGITQFQKGKEFEFAEGQGVPIAPGVPATEAKGYWYRHNRRSFKTADGN 115  
 SEQ ID NO: 6071 SGSVVPYYSWFSGITQFQKGKEFQFAEGQGVPIANGIPASEQKGYWYRHNRRSFKTPDGQ 118  
**SEQ ID NO: 6051 NT-----ASWFTALTQHGK-EELRFPRGQGVPIINTNSGPDDQIGYYRRATR-VRGGDGK 101**  
 SEQ ID NO: 6075 ----GNASWFQAIKAKKLNTPPPKFEGSGVPDNENIKPSQQHGYWR--RQARFKPGKGG 88  
 \* : : . \*\* . \*\* : : \*

SEQ ID NO: 6056 RVDLSPKLHFYYLGTGPHKDAKFRERVEGVVWVAVDGAKEPTGYGVRRKNSEPEIPHFN 130  
 SEQ ID NO: 6064 RIEQPSNWHFYYLGTGPHGDLRYRTRTEGVFWAKEGAKEPTNLGVRKASEKPIIPKFS 130  
 SEQ ID NO: 6060 RKELPERWFFYYLGTGPHADAKFKDKLDGVVWVAKDGAMNKPTTLGSRGANNESKALKFD 145

SEQ ID NO: 6068 QRQLLPWYFYLLGTGPHAKDQYGTIDIGVYVWASNQADVNTPADILDRDPSSD--EAIP 173  
 SEQ ID NO: 6071 QKQLLPWYFYLLGTGPHAGASYGDSIEGVFWVANSQADTNTRSDIVERDPSSH--EAIP 176  
**SEQ ID NO: 6051 MKELSPRWYFYLLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNN--AATV 159**  
 SEQ ID NO: 6075 RKPVPDAWYFYTTGTGPAADLNWGDQDQGVVWAAKGADTKSRNQGTDRDPDKF--DQYP 146

. \*\*\* \* : : \* : \* . . .

SEQ ID NO: 6056 QKLPNGVTVVEE---PDSRAPSRQSQR-----SQSRGRGESK----- 164  
 SEQ ID NO: 6064 QQLPSVVEIVEPNTPPASRANSRSRSGNGNNSRSPSNNRGNNQSRGNSQNRGNNQGRG 190  
 SEQ ID NO: 6060 GKVPGEFQLEVN---QSRDNSRSRQ-----SRSRSRNR----- 176  
 SEQ ID NO: 6068 TRFPPTVLPQGYIEGS-GRSAPNSR-----STSRASSRASS----- 210  
 SEQ ID NO: 6071 TRFAPGTVLPQGFYVEGS-GRSAPASR-----SGSRQSRRGP----- 212  
**SEQ ID NO: 6051 LQLPQGTTLPKGFYAEGSRGGSQASSR-----SSSRSGNSR----- 196**  
 SEQ ID NO: 6075 LRFSDGGPDGNFRWDFIPLNRGRSGRS-----TAASSAAASR----- 183

: . . . : . .

SEQ ID NO: 6056 -----PQSRNPSSDRNHN-----SQDDIMKAVAAALKSLGFDKPKQEKDKKS 205  
 SEQ ID NO: 6064 ASQNRGNNNNNNKSRNQSNRNQSNDRGGVTSRDDLVAAVKDALKSLGIGENPDRHKQ- 249  
 SEQ ID NO: 6060 -----SQSRGRQQFNKK-----DDSVQAVLAALKKLGVDTEKQQRS- 215  
 SEQ ID NO: 6068 -----AGSRSRANSNGRT-----PTSGVTPDMADQIASLVLAKLGKDAAKP 251  
 SEQ ID NO: 6071 -----NNRARSSSNQRQ-----PASTVKPDMAEEIAALVLAKLGKDAQP 252  
**SEQ ID NO: 6051 -----NSTPGSSRGNS-----PARMASGGGETALALLLLDRLNQLSKV 235**  
 SEQ ID NO: 6075 -----APSREGSRGR-----SDSGDDLIARAAKIIQDQ----- 212

. : .

SEQ ID NO: 6056 AKTGTPKPSRNQSPASSQTSKSLARSQSSETKEQKHEMQKPRWKRPNDVTSNVTQCF 265  
 SEQ ID NO: 6064 ----QKPKQEKSDNSGKNTPK---KNKSRATSKERDLKDIPWRRIPKG--ENSVAACF 300  
 SEQ ID NO: 6060 ----RSKSKERSNSKTRDTPK-----NENKHTWKRTAGK--GDVTRFY 253  
 SEQ ID NO: 6068 ----QVTKQTAKEIRQKILN-----KPRQKRPNK--QCTVQQCF 286  
 SEQ ID NO: 6071 ----KQVTKQSAKEVRQKILN-----KPRQKRTPNK--QCPVQQCF 287  
**SEQ ID NO: 6051 SGKGQQQQGTQVTKKSAEASK-----KPRQKRATK--QYNVTQAF 275**  
 SEQ ID NO: 6075 ----QKKGSRITKAKADEMAH-----RRYCKRTIPP--NYRVDQVF 247

: : \* \* :

SEQ ID NO: 6056 GPRDLH---NFGSAGVVANGVAKGYQFAELVPSTAAMLFDSSHIVSKESG----- 314  
 SEQ ID NO: 6064 GPRGGFK---NFGDAEFVEKGVDSGYAQIASLAPNVAALLFGGNVAVRELA----- 349  
 SEQ ID NO: 6060 GARSSA---NFGDTDLVANGSSAKHYPQLAECVPSVSSILFGSYWTSKEDG----- 302  
 SEQ ID NO: 6068 GKRGPNQ---NFGGSEMLKLGTSDPQFPILAEALAPTGAFFFGSRLELAKVQNLSGNLDE 343  
 SEQ ID NO: 6071 GKRGPNQ---NFGGSEMLKLGTSDPQFPILAEALAPTGAFFFGSKLELVKKN--SGGADE 342  
**SEQ ID NO: 6051 GRRGPEQTQGNFGDQDLIRQGTQYKHWPQIAQFAPSASAFFGMSRIGMEVTP----- 327**  
 SEQ ID NO: 6075 GPRTKGK-EGNFGDDKMNEEGIKDGRVTAMNLNLPSSHACLFGRVTPKLQL----- 298

\* \* \*\*\* . \* . . : . \* : : .

SEQ ID NO: 6056 ---NTVVLTFTRVTVPKDHP---HLGKFLEELNAFTR-----EMQ 349  
 SEQ ID NO: 6064 ---DSYEITYNYKMTVPKSDP---NVELLVSQVDAFKTGNALQQRKKEKKNKRETTLQ 401  
 SEQ ID NO: 6060 ---DQIEVTFTHKYHLPKDDP---KTGFLLQINAYAR-----PSEVAKEQR 343  
 SEQ ID NO: 6068 PQKDVYELRYNGAIRFDSTLSGFETIMKVLNENLNAYQQQD---GTMNMSPKPQRQ--R 397  
 SEQ ID NO: 6071 PTKDVYELQYSGAVRFDSTLPGFETIMKVLNENLNAYQKDG---GADVSPKPKRGRR 398  
**SEQ ID NO: 6051 ---SGTWLTYHGAIKLDDKDPQFKNVILLNKHIDAYKTFP---PTE----- 368**  
 SEQ ID NO: 6075 ---DGLHLRFEFTTVVPCDDPQFDNYVKICDQCVDGVGTRPKDDEPKPKSRSSSRPATRG 355

. : : . . . : .

SEQ ID NO: 6056 QHPLLNPFALEFNPSQTSP-----ATAEVRDEVSIEDIIDEVN----- 389  
 SEQ ID NO: 6064 QHEEAIYDDVGAPSDVTHANLEWDTAVDGGDTAVEIINEIFDTGN----- 446  
 SEQ ID NO: 6060 KRKSRSKSAERSEQDVVPDALIENYTDVFDQTQVEIIDEVTN----- 385  
 SEQ ID NO: 6068 GQKNGQGENDNISVAAPKSRVQKNKIRELTAEDISLLKKMDEP-----FTEDTSEI--- 448



SEQ ID NO:6071 QAEKKDEVNVSVAKPSSVQRNVSRELTPEDRSLLAQILDDGVVPDGLEDDSNV--- 454  
SEQ ID NO:6051 -PKDKKKKTDEAQPLPQRQKKQPTVTLTPAA----- 399  
SEQ ID NO:6075 NSPAPRQQRPKKEKKLKKQDDEADKALTSDEERNNAQLEFYDEPKVINWGDAALGENEL 414

FIGURE 7E

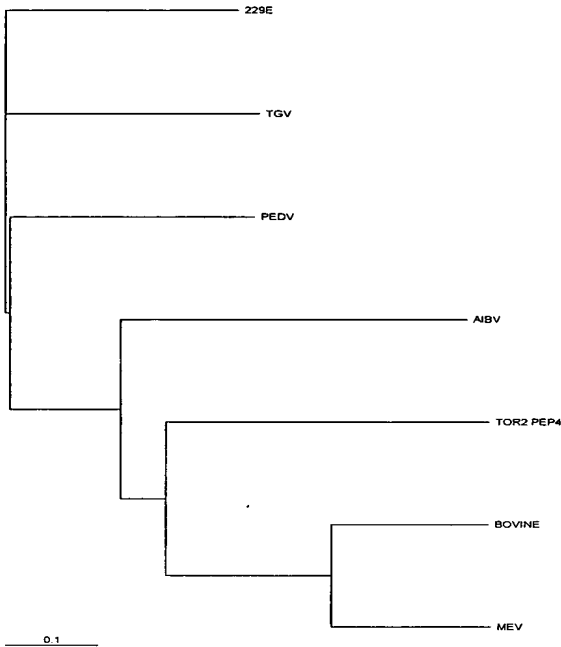
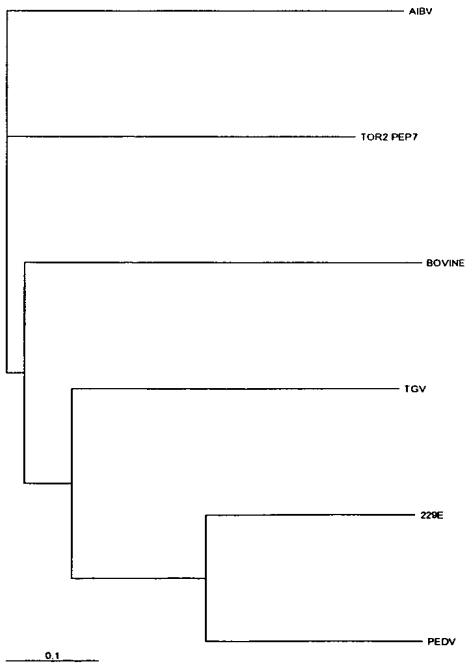
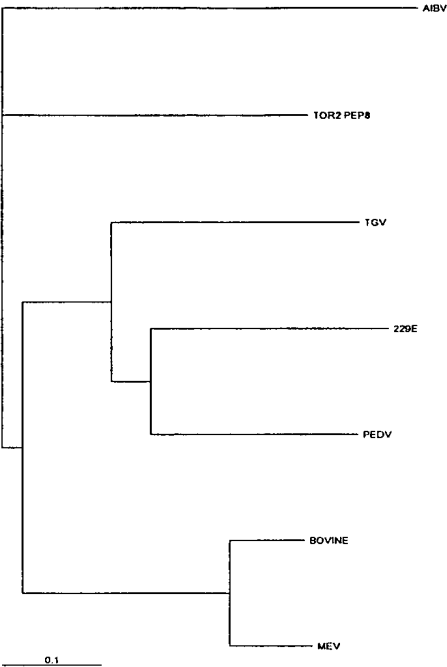


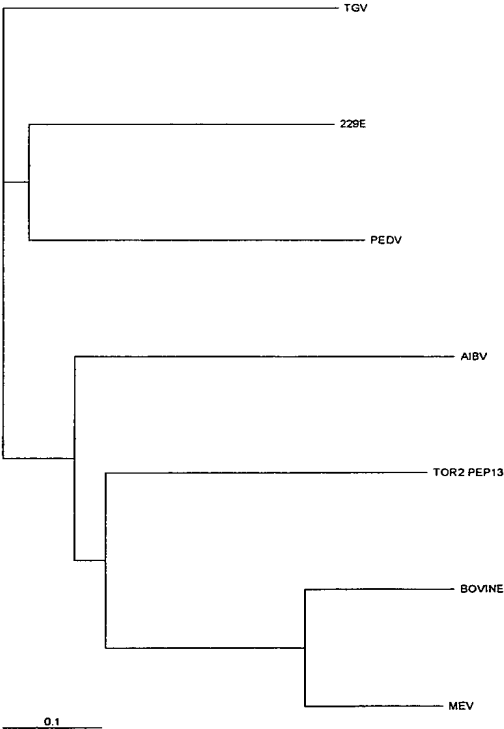
FIGURE 7F



**FIGURE 7G**



**FIGURE 7H**





**FIGURE 8**

						Section 1
	(1)	1	10	20	30	42
avian IBV partial 5'UTR 161-	(1)	TATTAAATCTTATTGTTGCTGGTATCACTGCTTGTGTTTGGCC				
HCoV-OC43 5'UTR	(1)	-----				
bovine CV 5'UTR	(1)	-----				
Consensus	(1)					
						Section 2
	(43)	43	50	60	70	84
avian IBV partial 5'UTR 161-	(43)	GTGTCTCACTTTATACATCTGTTGCTTGGGCTACCTAGTGTC				
HCoV-OC43 5'UTR	(1)	-----				
bovine CV 5'UTR	(1)	-----				
Consensus	(43)					
						Section 3
	(85)	85	90	100	110	126
avian IBV partial 5'UTR 161-	(85)	CAGCGTCCTACGGGCGTCGTGGCTGGTTCGAGTGCGAGGAAC				
HCoV-OC43 5'UTR	(1)	-----				
bovine CV 5'UTR	(1)	-----				
Consensus	(85)					
						Section 4
	(127)	127	140	150	168	
avian IBV partial 5'UTR 161-	(127)	CTCTGGTTTCATCTAGCGGTAGGCGGGTGTGTGGAAGTAGCA				
HCoV-OC43 5'UTR	(1)	-----GATTGTGACCGATTTCGCTGCGTGCA--TCCGGC				
bovine CV 5'UTR	(1)	-----GATTGCGAGCGATTTCGCTGCGTGCA--TCCCGC				
Consensus	(127)	GATTG GAGCGATTTCGCTGCGTGCA TCCCGC				
						Section 5
	(169)	169	180	190	200	210
avian IBV partial 5'UTR 161-	(169)	TTCAGACGTACCGGTTCTGTGTGTGAAATA--CGGGGTCA				
HCoV-OC43 5'UTR	(33)	TTCA-----CTGATCTCTTGTAGATCTTTTTGTAAATCTA				
bovine CV 5'UTR	(33)	TTCA-----CTGATCTCTTGTAGATCTTTTCATAATCTA				
Consensus	(169)	TTCA CTGATCTCTTGTAGATCTTTTCGTAATCTA				
						Section 6
	(211)	211	220	230	240	252
avian IBV partial 5'UTR 161-	(209)	CTCCCCCACATACCTCTAAGGGCTTTTGAGCCTAGCGTTGG				
HCoV-OC43 5'UTR	(68)	AACTTTATAAAAAACATCCACTCCCTGTAAATCTATGCTTGTGG				
bovine CV 5'UTR	(68)	AACTTTATAAAAAACATCCACTCCCTGTAGTCTATGCCTGTGG				
Consensus	(211)	AACTTTATAAAAAACATCCACTCCCTGTAGTCTATGCCTGTGG				
						Section 7
	(253)	253	260	270	280	294
avian IBV partial 5'UTR 161-	(251)	GCTACGTTCTCGCATAGGTCGGCTATACGACGTTTGTAGGG				
HCoV-OC43 5'UTR	(110)	GCGTAGATTTTTCATAGTGGTGTATATATT-CATTTCT-GCT				
bovine CV 5'UTR	(110)	GCGTAGATTTTTCATAGTGGTGTCTATATT-CATTTCT-GCT				
Consensus	(253)	GCGTAGATTTTTCATAGTGGTGTCTATATT CATTTCT GCT				
						Section 8
	(295)	295	300	310	320	336
avian IBV partial 5'UTR 161-	(293)	GGTAGTGCCAAACAAACCCCTGAGGTGACAGGTTCTGGTGGTG				
HCoV-OC43 5'UTR	(150)	GTTAACAGCTTTCAGCCAGGGACGTGTTGTATCCTAGGC---				
bovine CV 5'UTR	(150)	GTTAACAGCTTTCAGCCAGGGACGTGTTGTATCCTAGGC---				
Consensus	(295)	GTTAACAGCTTTCAGCCAGGGACGTGTTGTATCCTAGGC				
						Section 9
	(337)	337	350	360	373	
SEQ ID NO: 9910	(335)	TTTAGTGAGCAGACATACAATAGACAGTGACAAACATG				
SEQ ID NO: 9919	(189)	---AGTG-GCCCGCCCATAGGTCACAATG-----				
SEQ ID NO: 9892	(189)	---AGTG-GCCACCCCATAGGTCACAATG-----				
Consensus	(337)	AGTG GCCACCCCATAGGTCACAATG				

**FIGURE 9**

<b>SEQ ID NO:</b>		
F1: AT $\frac{CTT}{TGC}$ G $\frac{C}{A}$ G $\frac{GT}{CG}$ A $\frac{GGC}{TTT}$ G $\frac{G}{C}$ GTG	(136-154 nt)	<b>6021</b>
F2: GTG $\frac{T}{C}$ GTG $\frac{G}{C}$ AT $\frac{AG}{CC}$ C $\frac{A}{G}$ CTTCA	(152-172 nt)	<b>6022</b>
F3: CTTCAC $\frac{G}{T}$ G $\frac{T}{A}$ TCT $\frac{G}{C}$ TTGT $\frac{GT}{TA}$ GA	(168-195nt)	<b>6023</b>
R1: AG $\frac{A}{G}$ A $\frac{CCTGT}{TACAA}$ CAC $\frac{CTC}{G}$ $\frac{AGG}{CCT}$ GG $\frac{T}{C}$ TG	(307-329nt)	<b>6024</b>
R2: AAA $\frac{C}{T}$ G $\frac{CG}{AA}$ TATA $\frac{GC}{AA}$ C $\frac{GA}{AC}$ C $\frac{CT}{AC}$ TATG	(265-288nt)	<b>6025</b>
R3: C $\frac{GA}{AC}$ C $\frac{CT}{AC}$ TATG $\frac{CG}{AA}$ A $\frac{G}{A}$ A $\frac{A}{T}$ C $\frac{GTA}{TAC}$ GCCCA	(250-274nt)	<b>6026</b>

**FIGURE 10**

					Section 1	
	(1)	1	10	20	36	
avian IBV 3'UTR (NC_001451) 27103-	(1)	GTAACATAATGGACCTGTTGTTTCCTGGTACATTTT				
HCoV-OC43 3'UTR partial	(1)	-----				
bovine CV 3'UTR	(1)	-----				
Consensus	(1)					
					Section 2	
	(37)	37	50	60	72	
avian IBV 3'UTR (NC_001451) 27103-	(37)	GTAAACACTATTTCTGTGCTTTCCTATCAATTATT				
HCoV-OC43 3'UTR partial	(1)	-----				
bovine CV 3'UTR	(1)	-----				
Consensus	(37)					
					Section 3	
	(73)	73	80	90	108	
avian IBV 3'UTR (NC_001451) 27103-	(73)	ACAGGCATTGATTGTGATTATGTTCAATACTTAAGC				
HCoV-OC43 3'UTR partial	(1)	-----				
bovine CV 3'UTR	(1)	-----				
Consensus	(73)					
					Section 4	
	(109)	109	120	130	144	
avian IBV 3'UTR (NC_001451) 27103-	(109)	TTC TTTTGGTTGCTTTTGGCTTATTGTATTGTTGCT				
HCoV-OC43 3'UTR partial	(1)	-----				
bovine CV 3'UTR	(1)	-----				
Consensus	(109)					
					Section 5	
	(145)	145	150	160	170	180
avian IBV 3'UTR (NC_001451) 27103-	(145)	GTGCTTTTTATTGTTGTGATTCTCATTAGTTTG--G				
HCoV-OC43 3'UTR partial	(1)	-----TAAGAGAAATGAAC				
bovine CV 3'UTR	(1)	-----GAGAATGAAC				
Consensus	(145)	A GAGAATGAAC				
					Section 6	
	(181)	181	190	200	216	
avian IBV 3'UTR (NC_001451) 27103-	(179)	TTTATCGTAGAAATTCAATAGTAAGAGTTAAGGAAG				
HCoV-OC43 3'UTR partial	(14)	CTTAT-GTCGGCACCTGGTGGTAACCCCTC-GCAGG				
bovine CV 3'UTR	(11)	CTTAT-GTCGGCACCTGGTGGTAACCCCTC-GCAGG				
Consensus	(181)	CTTAT GTCGGCACCTGGTGGTAACCCCTC GCAGG				
					Section 7	
	(217)	217	230	240	252	
avian IBV 3'UTR (NC_001451) 27103-	(215)	ATAGGCATGTAGCTTGATTACCTACATGTCTATCGC				
HCoV-OC43 3'UTR partial	(48)	AAAGTCGGG-----ATAAGGCAC-TCTCTATCAG				
bovine CV 3'UTR	(45)	AAAGTCGGG-----ATAAGGCAC-TCTCTATCAG				
Consensus	(217)	AAAGTCGGG ATAAGGCAC TCTCTATCAG				

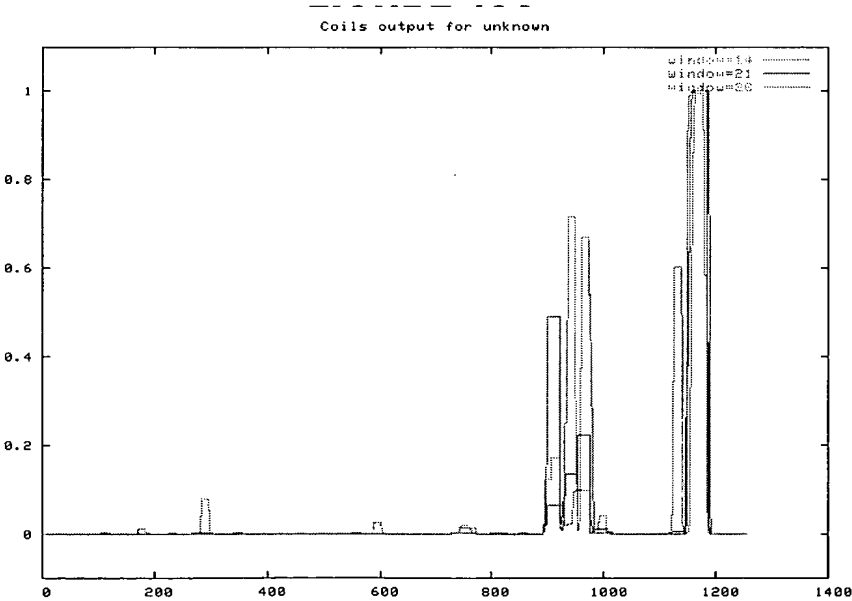
**FIGURE 10 (contd.)**

					Section 8	
	(253)	253	260	270	288	
avian IBV 3'UTR (NC_001451) 27103-	(251)	CAGCGGA	AAATGCTCTAATCTGTCTACTTAGTAGCCTGG			
HCoV-OC43 3'UTR partial	(76)	AATCGA	--TGTCTTGCTGCTATAATAGATAGA---	G		
bovine CV 3'UTR	(73)	AATCGA	--TGTCTTGCTGCTATAATAGATAGA---	G		
Consensus (253)		AATGGA	TGTCTTGCTGCTATAATAGATAGA		G	
					Section 9	
	(289)	289	300	310	324	
avian IBV 3'UTR (NC_001451) 27103-	(287)	AAACGAACGCTAGACCC	TTAGATTTTAATTTAGTTT			
HCoV-OC43 3'UTR partial	(107)	AAGGTTATAGCAGACTAT	-AGATT---	AATTAGTTG		
bovine CV 3'UTR	(104)	AAGGTTATAGCAGACTAT	-AGATT---	AATTAGTTG		
Consensus (289)		AAGGTTATAGCAGACTAT	AGATT	AATTAGTTG		
					Section 10	
	(325)	325	330	340	350	360
avian IBV 3'UTR (NC_001451) 27103-	(323)	AAATTTTAGTTT	TAAGTTAGT-TTAGAGTAGG			
HCoV-OC43 3'UTR partial	(139)	AAAGTTTGTGTGCTAATGTATAGTGT	TGGCAGAAAG			
bovine CV 3'UTR	(136)	AAAGTTTGTGTGCTAATGTATAGTGT	TGGCAGAAAG			
Consensus (325)		AAAGTTTGTGTGCTAATGTATAGTGT	TGGCAGAAAG			
					Section 11	
	(361)	361	370	380	396	
avian IBV 3'UTR (NC_001451) 27103-	(358)	TATAAAGATGCCAGT	GGCGGGCCAC-GCGGAGTAC			
HCoV-OC43 3'UTR partial	(175)	TG-AAAGACT---	TGGGGAAGTAATTGCCGACAAG			
bovine CV 3'UTR	(172)	TG-AAAGACT---	TGGGGAAGTAATTGCCGACAAG			
Consensus (361)		TG AAAGACT	TGGGGAAGTAATTGCCGACAAG			
					Section 12	
	(397)	397	410	420	432	
avian IBV 3'UTR (NC_001451) 27103-	(393)	GATCGAGGGTACAGCACTAGGACG	CCCCATTAGGGGA			
HCoV-OC43 3'UTR partial	(206)	TGCCCAAAGGGGAAGAGCCAGCACG	----	TTAAGTTA		
bovine CV 3'UTR	(203)	TGCCCAAAGGGGAAGAGCCAGCATG	----	TTAAGTTA		
Consensus (397)		TGCCCAAAGGGGAAGAGCCAGCACG		TTAAGTTA		
					Section 13	
	(433)	433	440	450	468	
avian IBV 3'UTR (NC_001451) 27103-	(429)	AGAGCTAAATTTAGT--TTAAGTTAAGTTTAAAT-T				
HCoV-OC43 3'UTR partial	(238)	CCACCCAGTAATTAGTAAATGAATGAAGTTAATTAT				
bovine CV 3'UTR	(235)	CCATCCAGTAATTAGTAAATGAATGAAGTTAATTAT				
Consensus (433)		CCA CCAGTAATTAGTAAATGAATGAAGTTAATTAT				
					Section 14	
	(469)	469	480	490	504	
avian IBV 3'UTR (NC_001451) 27103-	(462)	GGCTAAGTATAGTTAAAATTTATAGGCTAGTATAGA				
HCoV-OC43 3'UTR partial	(274)	GGCCAATTGGAAGAATCAC-				
bovine CV 3'UTR	(271)	GGCCAATTGGAAGAATCAC-				
					Section 15	
	(505)	505	513			
avian IBV 3'UTR (NC_001451) 27103-	(498)	GTTAGAGCA		SEQ ID NO: 9911		
HCoV-OC43 3'UTR partial	(293)	-----		SEQ ID NO: 9920		
bovine CV 3'UTR	(290)	-----		SEQ ID NO: 9893		
Consensus (505)						

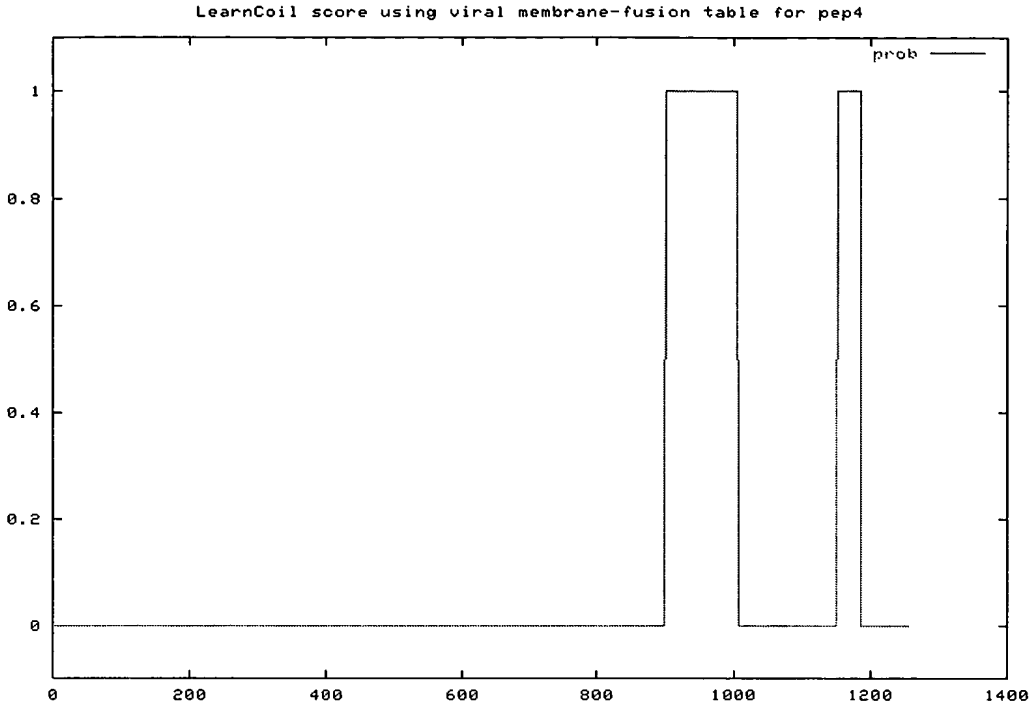
FIGURE 11

SEQ ID NO:		
F-1	TCTATC $\frac{GCC}{AGA}$ A $\frac{G}{T}$ GGATGTCT (245 ~ 265 nt)	6027
F-2	TTAGTT $\frac{T}{G}$ AA $\frac{TT}{AG}$ TTT $\frac{A}{T}$ GT $\frac{T}{G}$ T $\frac{A}{G}$ GT (318 ~ 339 nt)	6028
F-3	TAGTGTT $\frac{A}{G}$ GAG $\frac{T}{A}$ A $\frac{G}{A}$ GT $\frac{A}{G}$ TAAAGA (346 ~ 368 nt)	6029
R-1	A $\frac{A}{C}$ TT $\frac{G}{A}$ GCCATA $\frac{A}{T}$ T $\frac{T}{A}$ AACTT (458 ~ 476 nt)	6030
R-2	ACTAA $\frac{TTAC}{AATT}$ T $\frac{G}{A}$ $\frac{C}{T}$ $\frac{GG}{CT}$ T $\frac{AA}{CC}$ C $\frac{T}{C}$ TAA (426 ~ 448 nt)	6031
R-3	T $\frac{TG}{AC}$ TC $\frac{G}{C}$ GC $\frac{AA}{G}$ T $\frac{TA}{GG}$ C $\frac{TT}{CC}$ C $\frac{C}{G}$ GCA (375 ~ 395 nt)	6032 6033

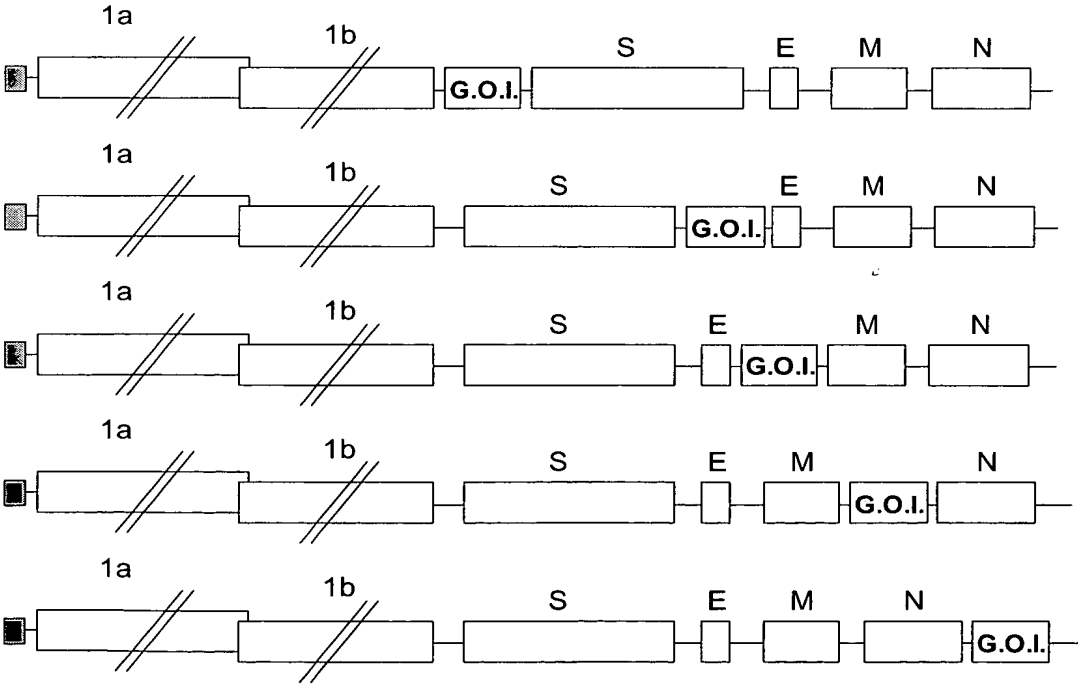
FIGURE 12



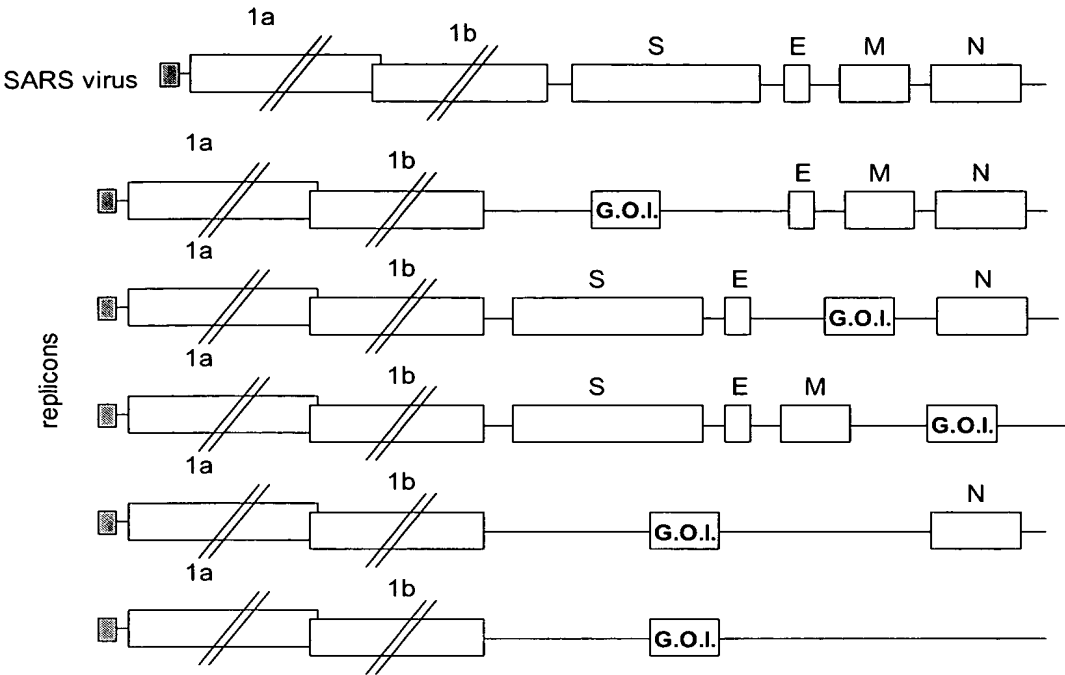




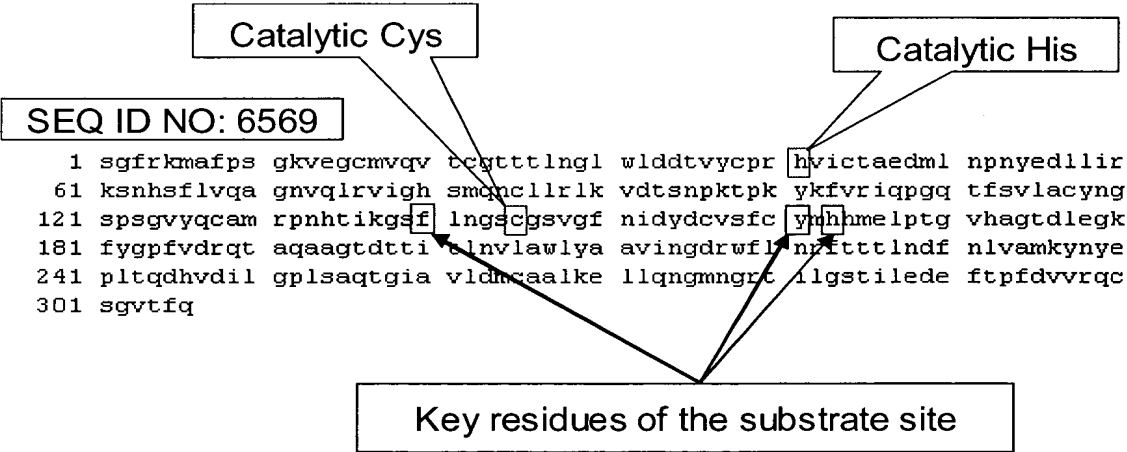
**FIGURE 13**



**FIGURE 14**



**FIGURE 15**



**FIGURE 16**

										Section 1		
	(1)	1	10	20	30	40	51					
avian IBV nsp2	(1)	SGFKK	VSP	SAVEK	CIVSV	YRCNN	LNGLWLGD	YCPR	V	G	---KF	G
MHV nsp2	(1)	SG	VKMVSP	SKVEPC	IVSV	TYGN	MTLNGLWLDD	DKVYCP	RVICS	DMTD		
SARS nsp2	(1)	SGFRKMAFP	GKVEGC	VQVTC	GTTT	LNGLWLDD	VYCP	RVICS	AEDMLN			
BCoV nsp2	(1)	SG	VKMVNF	SKVEPC	IVSV	TYGN	MTLNGLWLDD	DKVYCP	RVICSA	DMTN		
Consensus	(1)	SGIVKMVSPSSKVEPCIVSVTYGNMTLNGLWLDDTVYCPRVICSAADMTN										
Section 2												
	(52)	52	60	70	80	90	102					
avian IBV nsp2	(49)	DQ	ND	LNLANNH	FEVT	QHGV	LVN	SRR	KGA	L	LQTA	ANAETPKY
MHV nsp2	(52)	PDYP	LLCRVT	DPCV	GR	SLTVMSYQM	QGC	LVLT	TVTLQNP	TPKY		
SARS nsp2	(52)	PNYEDLLIRK	NHSFLVQAGN	VQLRV	G	SMQNC	LRLK	VDT	SNP	TPKY		
BCoV nsp2	(52)	PDYT	LLCRVT	DFTV	FDR	SLTVMSYQM	QGC	LVLT	TVTLQNS	TPKY		
Consensus	(52)	PDY	NLLCRVTSSDF	VLSGR	VSLTVMSYQM	QGC	LLVLT	TVTLQNP	KTPKY			
Section 3												
	(103)	103	110	120	130	140	153					
avian IBV nsp2	(100)	KFIKANCG	FT	ACAYGG	VVGL	PVTMR	SNGTI	SS	LAG	CGSVG	N	
MHV nsp2	(102)	SFGVVKPG	ETFTVLAAYNGR	PQGA	HVT	RS	HTIKGS	FLCGS	CGSVG			
SARS nsp2	(102)	KFVR	QPGQTF	VLACYNG	PSGV	QCAMR	PNHTIKGS	LNCS	CGSVG	N		
BCoV nsp2	(102)	TFGVVKPG	ETFTVLAAYNGK	PQGA	HVTMR	S	TIKGS	FLCGS	CGSVG			
Consensus	(103)	KFGVVKPG	ETFTVLAAYNGSPQGA	FHVTMR	SSHTIKGS	FLCGS	CGSVG	FVI				
Section 4												
	(154)	154	160	170	180	190	204					
avian IBV nsp2	(151)	KGVVNF	FVM	HLELPN	LHTGTD	MG	FYGGYVDEEVA	AQRVPPDN	LV	TNN		
MHV nsp2	(153)	TGDSV	FVVM	HLEL	TGCHTGT	DFSGNFYGPYRDAQV	QLPVQDY	TQTVN				
SARS nsp2	(153)	YDCV	SFCYM	HLELP	TGVHAGTD	EGKFYGP	VDRQTAQAAGT	DTTIT	N			
BCoV nsp2	(153)	MGDCV	FVVM	HLEL	TGCHTGT	DFNG	FYGPYKDAQV	QLPVQDY	IQ	VN		
Consensus	(154)	DGDCV	KFVVMHQL	ELSTGCHTGTDL	GDFYGPYVDAQV	QLPVQDY	TQTVN					
Section 5												
	(205)	205	210	220	230	240	255					
avian IBV nsp2	(202)	VVAWLYAAI	ISVK	ESSFSLPK	ESTTVS	ED	NKWAGDNGF	PFS	S	--T		
MHV nsp2	(204)	VVAWLYAAI	FNRCN	----	WFLQSD	CS	E	FNWAM	NGFSS	KAD	--L	
SARS nsp2	(204)	V	AWLYAA	INGDR	----	WFL	RFTT	INDFN	VAMKYN	EP	TQDHVD	
BCoV nsp2	(204)	FVAWLYAAI	NNCN	----	WFLQSD	KCS	EDFNWAM	NGFSQ	K	D	--L	
Consensus	(205)	VVAWLYAAI	IN CN		WFLQSD	TCS	LED	FNWAM	SNGF	SPIKSD	L	
Section 6												
	(256)	256	270	280	290	306						
avian IBV nsp2	(251)	A	TKLS	TGVDV	CKLLRTIMV	KNS-Q	GGDPILGQYN	FEDELTP	ESV	Q		
MHV nsp2	(247)	V	DAL	MTGV	VEQ	LAAIKRLHS	-GFOG	QILGSC	FEDELTP	SDVYQQ		
SARS nsp2	(249)	G	PL	QOTG	AVLD	CAA	KELLQNGM	GR	TILGST	FEDEFT	PFEDVVRQ	
BCoV nsp2	(247)	V	DAL	MTGV	ETLLAAIKRLKN	-GFOGRQI	GS	CS	FEDELTP	SDVYQQ		
Consensus	(256)	VIDALAAM	TGVSV	LLAAIKRL	S	GFOGRQI	L	GS	CILEDELTP	SDVYQQ		
Section 7												
	(307)	307	313									
avian IBV nsp2	(301)		GV	LQ	SEQ ID NO: 6570							
MHV nsp2	(297)		LAGVK	LQ	SEQ ID NO: 6571							
SARS nsp2	(300)		C	GVTFQ	SEQ ID NO: 6569							
BCoV nsp2	(297)		LAG	KLQ	SEQ ID NO: 6572							
Consensus	(307)		LAGVK	LQ	SEQ ID NO: 6573							

FIGURE 17

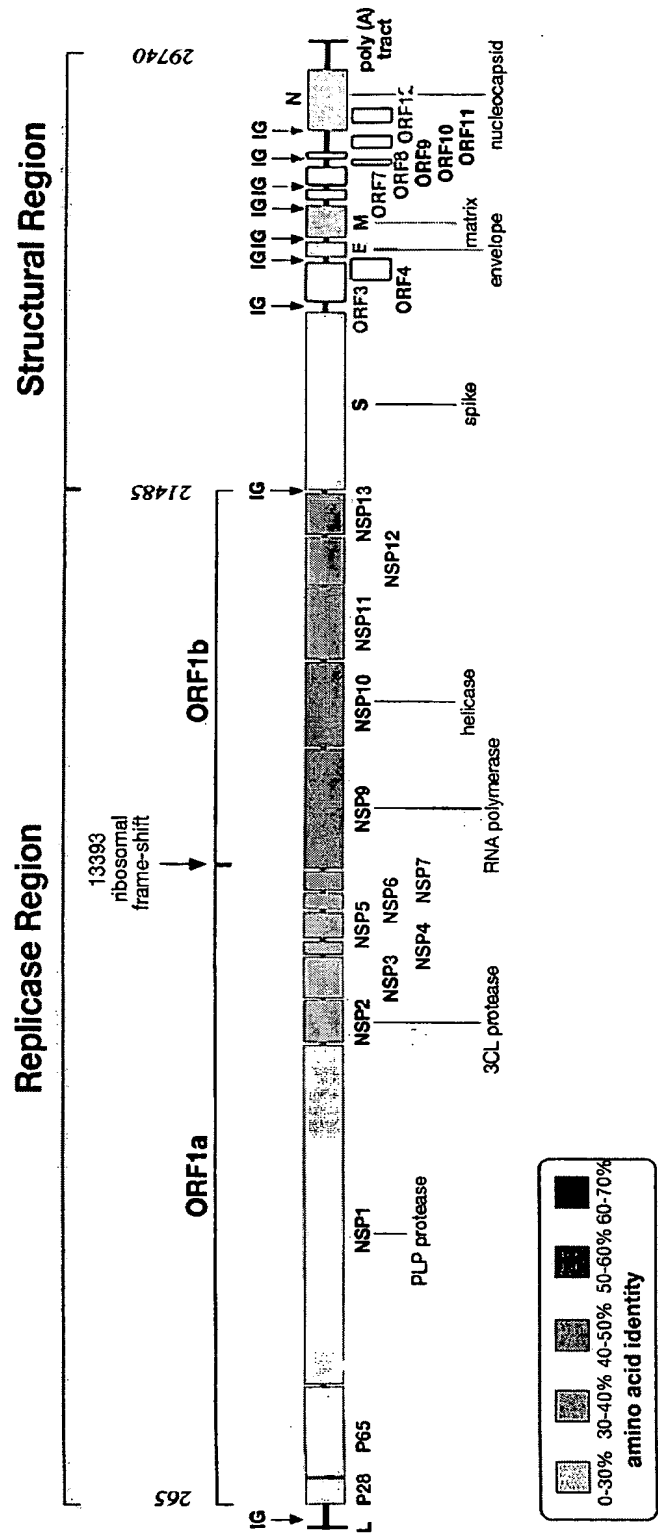
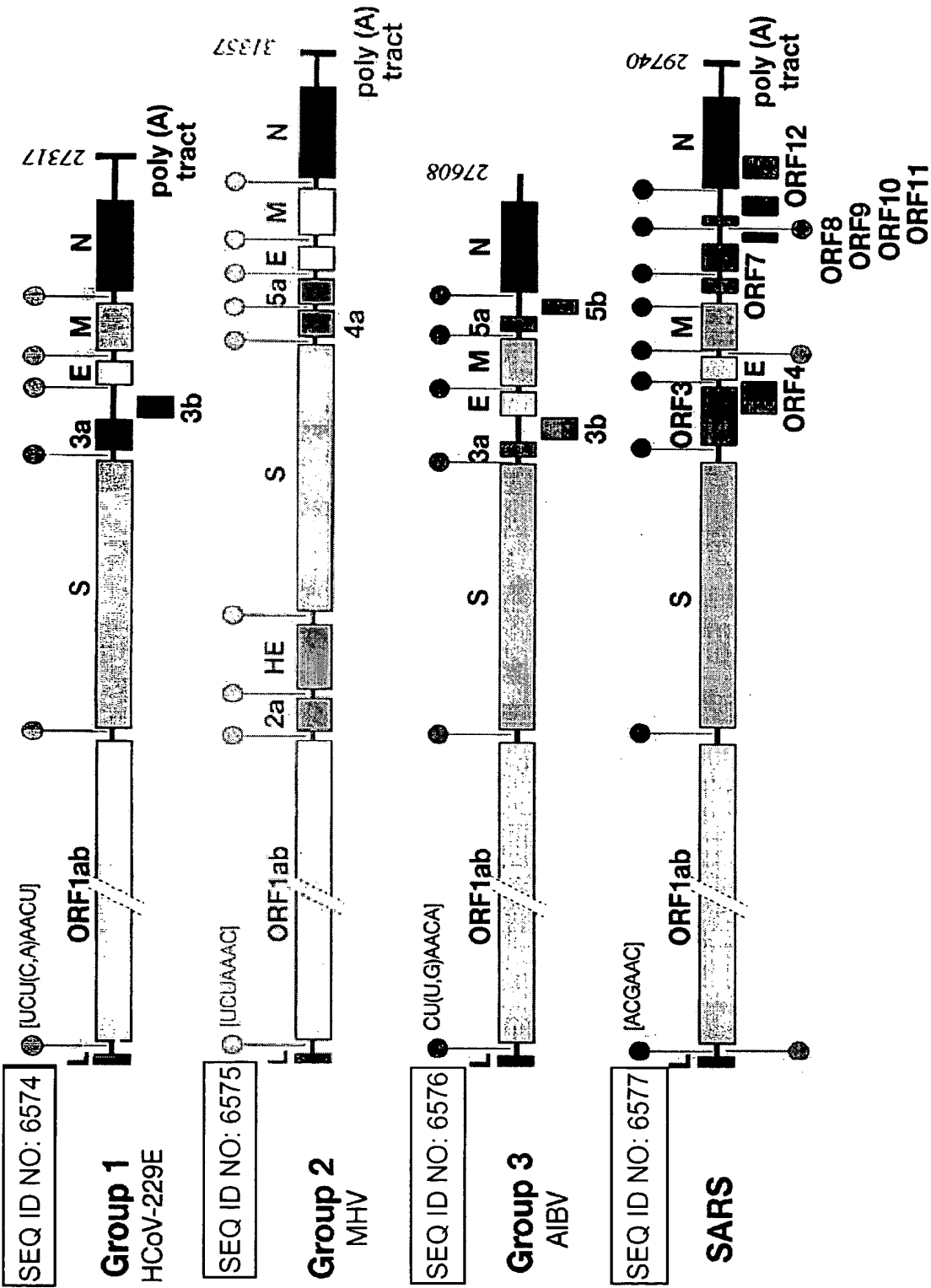


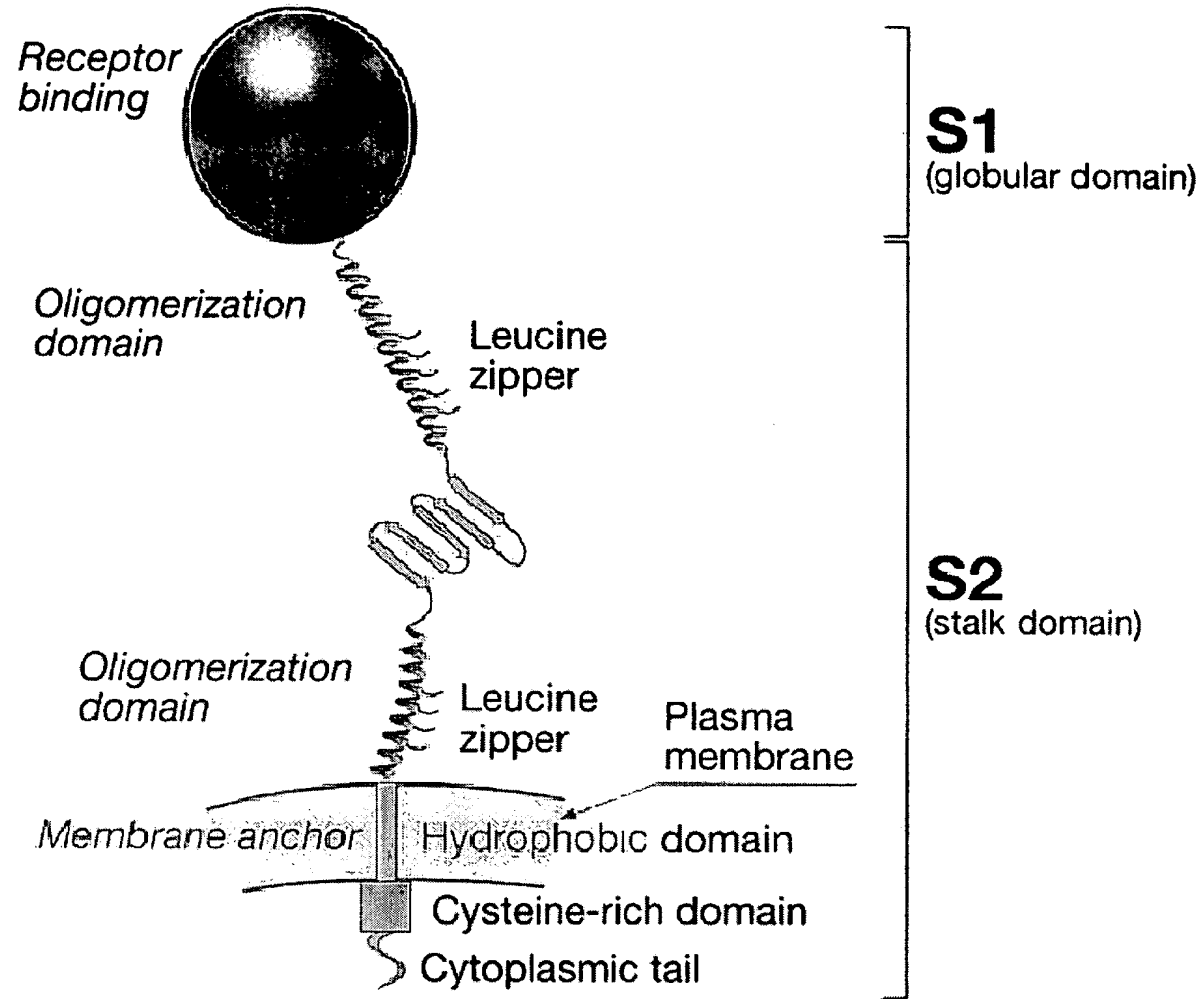
FIGURE 18

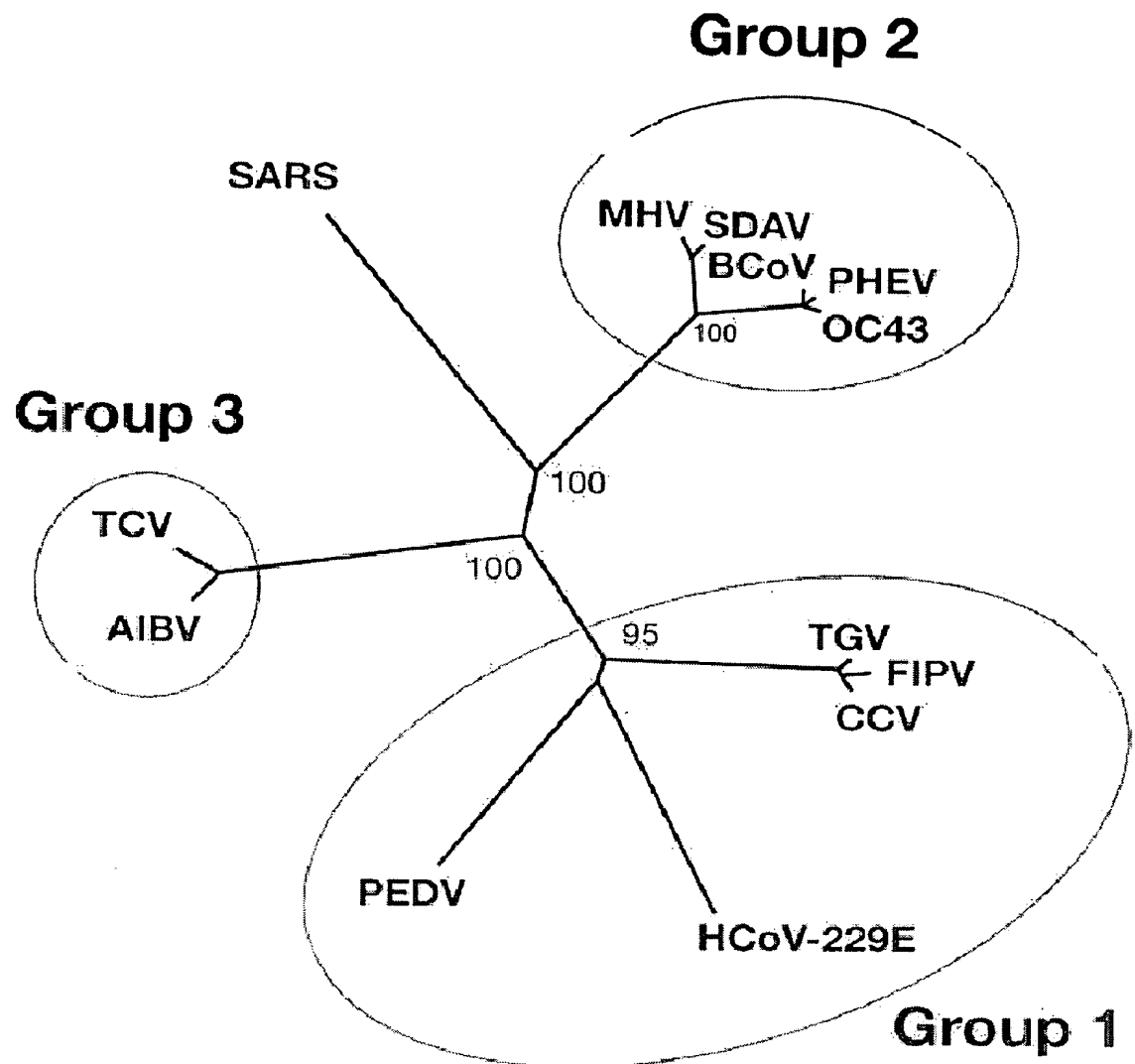


**FIGURE 19**

**FUNCTION**

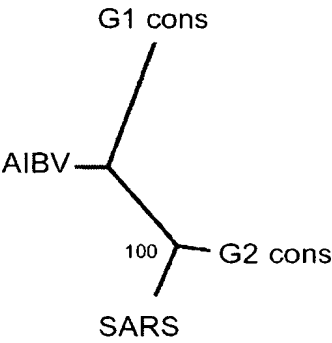
**STRUCTURE**



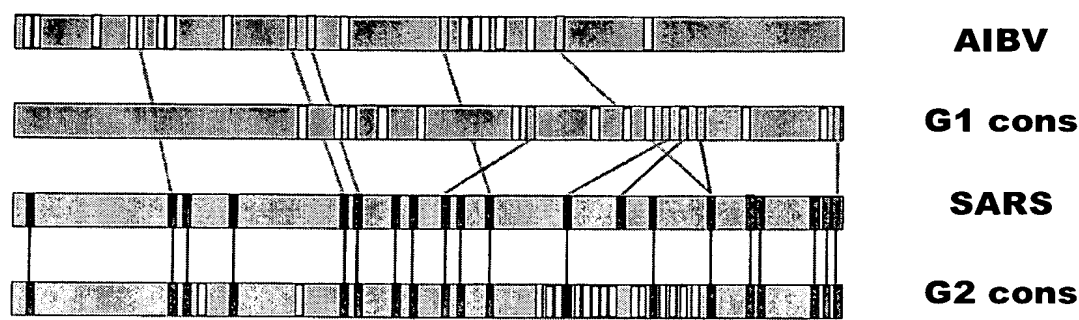
**FIGURE 20**

**FIGURE 21**

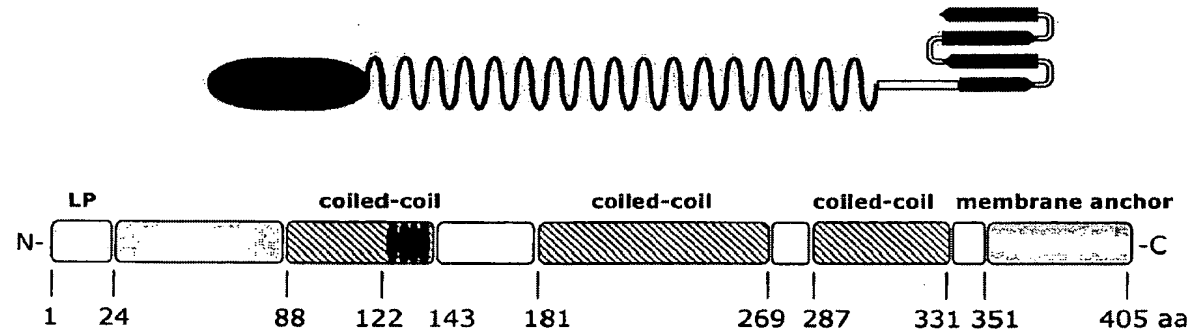
**FIGURE 21A**



**FIGURE 21B**



**FIGURE 22**





**FIGURE 23**

LPRKSQPTSISCRSVL-TNFKICVAVARLHA-CTYAV-TIINFTVVDKKRVTRPSSADCL  
 RFRPCCSRSSAYLGFVRV-PKGKMESLVLGVNEKTHVQLSLPVLQVRDVLVRGFGDSVEE  
 ALSEAREHLKNGTCGLVELEKGVLPQLEQPYVFIKRS DALSTNHGHKVVELVAEMDGIQY  
 GRSGITLGLVLPVHGETPIAYRNVLLRKNNGKAGGHSYGIDLKSYDLGDELGTDPIEDY  
 EQNWNTKHGSGALRELTRELNGGAVTRYVDNNFCGPDGYPLDCIKDFLARAGKSMCTLSE  
 QLDYIESKRGVYCCRDHEHEIAWFTERSDKSYEHQTPFEIKSAKKFDTFKGECPKFVFPL  
 NSKVKVIQPRVEKKKTEGFMGRIRSVYPVASPQECNNMHLSTLMKCNHCDEVSWQTCDFL  
 KATCEHCGTENLVIEGPTTCGYLPTNAVVKMPCPACQDPEIGPEHSVADYHNHSNIETRL  
 RKGGRTRCFGGCVFAYVGCYNKRAYWVPRASADIGSGHTGITGDNVETLNEDLLEILSRE  
 RVNINIVGDFHLNEEVAIILASFSASTSAFIDTIKSLDYKSFKTIVESCGNYKVTKGKPV  
 KGAWNIGQQRSVLTPLCGFPSQAAGVIRSI FARTLDAANHSIPDLQRAAVTILDGISEQS  
 LRLVDAMVYTSDDLNTSVIIMAYVTGGLVQOTSQWLSNLLGTTVEKLRPIFEWIEAKLSA  
 GVEFLKDAWEILKFLITGVFDIVKGQIQVASDNIKDCVKCFIDVNVKALEMCIQVITIAG  
 AKLRSLNLGEVFIAQSKGLYRQCIRGKEQLQLLMPLKAPKEVTFLEGDSHDTVLTSEEVV  
 LKNGELEALETPVDSFTNGAIVGTPVCVNGMLMLEIKDKEQYCALSPGLLATNNVFRKLG  
 GAPIKGVTFGEDTVWEVQGYKNVRITFELDERVDKVLNEKCSVYTVESGTEVTEFACVVA  
 EAVVKTLQPVSDLLTNMGIDLDEWSVATFYLFDDAGEENFSSRMYSFYPPDEEEEDDAE  
 CEEEEIDETCEHEYGTEDDYQGLPLEFGASAETVRVEEEEEEDWLDDTTEQSEIEPEPEP  
 TPEEPVNQFTGYLKLTDNVAIKCVDIVKEAQSANPMVIVNAANIHLKHGGGVAGALNKAT  
 NGAMQKESDDYIKLNGPLTVGGSCLLSGHNLAKKCLHVVGPNLNAGEDIQLLKAAYENFN  
 SQDILLAPLLSAGIFGAKPLQSLQVCVQTVRTQVYIAVNDKALYEQVVM DYLDNLKPRVE  
 APKQEEPPNTEDSKTEESVQKPVDPVKPKIKACIDEVTTTLEETKFLTNNKLLLFADING  
 KLYHDSQNMLRGEDMSFLEKDAPYMGDVITSGDITCVVI PSKKAGGTTEMLSRALKKVP  
 VDEYITTYPGQGCAGYTLEEAKTALKKCKSAFYVLPSEAPNAKEEILGTVSWNLREMLAH  
 AEETRKLMPICMDVRAIMATIQRKYKGIKIQEGIVDYGVRFFFTYSKEPVASIIITKLNSL  
 NEPLVTMPIGYVTHGFNLEEAARCMRSLKAPAVSVSSPDVTTYNGYLTSSSKTSEEHF  
 VETVSLAGSYRDWSYSGQRTELGVFELKRGDKIVYHTLES PVEFHLDG EVLSLDKLSLL  
 SLREVKTIKVFTTVDNNTNLHTQLVDMSMTYGGQFGPTYLDGADVTKIKPHVNHEGKTFV  
 LPSDDTLRSEAFEYYHTLDESFLGRYMSALNHTKKWKFPQVGGLTSIKWADNNCYLSSVL  
 LALQQLEVKFNAPALQEAYYRARAGDAANFCALILAYSNKTVGELGDVRETMTHLQHAN  
 LESAKRVLNVVCKHCGQKTTTLTGVEAVMYMGTLSDNLKTGVSI PCVCGRDATQYLQQ  
 ESSFVMMSAPPAEYKLQQGTFLCANEYTGNYQCGHYTHITAKETLYRIDGAHLTKMSEYK  
 GPVTDVIFYKETS YTTTIKPVSYKLDGVTYTEIEPKLDGYKKNAYYTEQPIDLVPTQPL  
 PNASFDNFKLTCSNTKFADDLNQMTGFTKPA SRELSVTFFPDLNGDVVAIDYRHYSASF  
 KGAKLLHKPIVWHINQATTKTTFKPNTWCLRCLWSTKPVDTSNSFEVLAVEDTQGM DNLA  
 CESQQPTSEEVVENPTIQKEVIECDVKTTEVVG NVILKPSDEGVKVTQELGHEDLMAAYV  
 ENTSITIKKPNELSLALGLKTIATHGIAAINSVPWSKILAYVKPFLGQAAITTSNCAKRL  
 AQRVFNNYMPYVFTLLFQLCTFTKSTNSRIRASLP TTI AKNSVKSVAKLCLDAGINYVKS  
 PKFSKLFTIAMWLLLLSICLGS LICVTA AFGVLLSNFGAPSYCNGVRELYLNSSNVTTMD  
 FCEGSFPCSI CLSGLDSLDSYPALETIQVTISSYKLDLTIILGLAAEWV LAYMLFTKFFYL  
 LGLSAIMQVFFGYFASHFISNSWLMWFIISIVQMAPVSAMVRMYIFFASFYIWKSYVHI  
 MDGCTSS TCMCYKRN RATRVECTTIVNGMKRSFYVYANGGRGFCKTHNWNCLNCDT FCT  
 GSTFISDEVARDLSLQFKRPINPTDQSSYIVDSVAVKNGALHLYFDKAGQKTYERHPLSH  
 FVNLDNLRANNTKGS LPINVI VFDGKSKCDESASKSASVYYSQLMCQPILLLDQALVSDV  
 GDSTEVSVKMFDAYVDTFSATFSVPMEKLKALVATAHSELAKGVALDGVLSTFVSAARQG  
 VVDTDVDTKD VIECLKLSHSDLEVTDGSCNNFMLTYNKVENMTPRDLGACIDCNARHIN  
 AQVAKSHNVSLIWNVKDYMSLSEQLRKQIRSA AKKNNI PFRLTCATTRQVVNVIITTKISL  
 KGGKIVSTCFKLMLKATLLCVLAALVCYIVMPVHTLSIHDGYTNEIIGYKAIQDGVTRDI  
 ISTDDCFANKHAGFDAWFSQRGGSYKNDKSCPVVAAIITREIGFIVPGLPGTVLRAIN GD  
 FLHFLPRVFSAVGNICYTPSKLIEYSDFATSACVLAAECTIFKDAMGKPVPCYDNTLLE  
 GSISYSELRPDTRYV LMDGSI IQFPNTYLEGSRVRVTTFDAEYCRHGT CERSEVGICLST  
 SGRWVLNNEHYRALSGVFCGV DAMNLIANIFTPLVQPVGALDVSASVAGGIIAILVTCA  
 AYYFMKFRRVFGEYNHVVAANALLFLMSFTILCLVPAYSFLPGVYSVFYLYLTFYFTNDV

SFLAHLQWFAMFSPIVPFWITAIYVFCISLKHCHWFFNNYLKRKRVMFNGVTFSTFEEAAL  
CTFLLNKEMYLKLRSETLLPLTQYNRYLALYNKYKYFSGALDTSYREAACCHLAKALND  
FSNSGADVLYQPPQTSITSAVLQSGFRKMAFPSGKVEGCMVQVTCGTTTTLNGWLDDTVY  
CPRHVICTAEDMLNPNYEDLLIRKSNHSFLVQAGNVQLRVIGHSMQNCLLRLKVDTSNPK  
TPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMPNHTIKGSFLNGSCGSGVFNIDYDCV  
SFCYMHMELPTGVHAGTDLEGKFYGPFDVDRQTAQAAGTDTTITLNVLAWLYAAVINGDR  
WFLNRFTTTLNDENLVAMKYNYEPLTQDHVDILGPLSAQTGIAVLDMCAALKELLQNGMN  
GRTILGSTILEDEFTPFDDVVRQCSGVTFQGKFKKIVKGTHHWMLLTFLTSLILVQSTQW  
SLFFFVYENAFLPFTLGIMAIAACAMLLVKHKAFLCLFLLPSLATVAYFNMVYMPASWV  
MRIMTWLELADTSLSGYRLKDCVMYASALVLLILMTARTVYDDAARRVWTLNMVITLVYK  
VYYGNALDQAI SMWALVISVTSNYSGVVTTIMFLARAI VFVCVEYYPLL FITGNTLQ CIM  
LVYCFGLGYCCCCYFGLFCLLNRYFRLTLGVYDYL VSTQEF RYMNSQGLLPKSSIDAFKL  
NIKLLGIGGKPCIKVATVQSKMSDVKCTSVVLLSVLQQLRVESSSKLWAQCVQLHNDILL  
AKDTTEAFEKMSVLLSVLLSMQGAVDINRLCEEMLDNRATLQAIASEFSSLP SYAAYATA  
QEAYEQAVANGDSEVVLKLLKKS LNVAKSEFDRDAAMQRKLEKMAQAMQMYKQARSED  
KRAKVT SAMQTM LFTMLRKL DNDALNNI INNADGCVPLNI I PLTTAAKLMVVVPDYGT Y  
KNTCDGNTFTYASALWEIQQVVDADSKI VQLSEINMDNSPNLAWPLIVTALRANS AVKLQ  
NNELSPVALRQMSCAAGTTQTACTDDNALAYNNSKGGRFVLALLSDHQDLKWARFPKSD  
GTGTIYTELEPPCRFVTDTPKGPKVKYLYFIKGLNNLNRGMVLGSLAATVRLQAGNATEV  
PANSTVLSFCAFAVDPAKAYKDYLASGGQPITNCVKMLCTHTGTGQAITVTPEANMDQES  
FGGASCCLYCRCHIDHPNPKGFCDLKGKYVQIPTTCANDPVGFTLRNTVCTVCGMWKGYG  
CSCDQLREPLMQSADASTFLNGFAV-VQPV LHRAAQALV LMSSTGLLI FTTKLLVLQSS  
-KLI AVASRRMRKAIY-TLTL-LRGILCLTTNMKRLFITWLKIVQRLLSMTFSSLE-MV  
TWYHIYHVS V-LNTQWLI-SMLYVILMRVIVIH-KKYSSHTIAVMMIISIRRIGMTS-RI  
LTSYAYMLT-VSVYANHY-RLYNSAMLCVMQAL-AY-H-IIRILMGTGTISVISYK-HQA  
AEFLLWIHITHC-CPSSL-LGHWLLSPIWMLISQNHLLSGIC-NMILRKRDFVSSTVILN  
IGTRHTIPIVLTVMIGVSFIVQTLMCYFLLCFHLQVLDH--EKYL-MVFLLLFQLD TIF  
VS-ESYIIRM-TYIARVSVRNF-CMLLIQLCMQLLAIYC-INALHAFQ-LH-QTMLLFK  
LSNPVILIKTFMTLLCLKVSLRKEVLLN-NTSSLLRMATLLSVIMTIIVIICQQCVISDN  
SYS-LKLLINTLIVTMVAVLMPTK-SLTIWINQLVSHLINGVRLDFIMTQ-VMRIKMHS  
RILSVMSLL-LK-ILSMPLVQRIELAP-LVSLSVVL-QIDSFIRNY-SQ-PPLEELLW-  
LEQASFTVAGIIC-KLFTVM-KLHTLWVGIIQNVTEPCLTCLG-WPLLFLLANITLAVTY  
HTVSTG-LTSVRKY-VRWSCVAAHYMLNQVEHHPVMLQLLMLIVSLTFVKLLQPM-MHFF  
QLMVIR-LTSM SAIYNTGSM SVSIEIGMLIMNSWMSFTLT CVNISP--FFLMPLCAITV  
TMRLKV--LALRTL RQFFIIKIMC SCLRQNVGLRLTLKDLTNFAHSIQC-LNKEMITCT  
CLTQIHQ EY-AQAVLSMILSKQMVHL-LKGSCHWLLMLTHLQNILIRSM LMSFTCIYNTL  
ESYMSLLATCWT CIP-C-LMITPHGTGNLSFMRLCTHHIQSCRL-VLVYCAIHR LH FVA  
VPVLGDHSYVASAAMTMSFQHHTN-CCLLIPMFAMPQVVM SLM-HNCI-EV-AIIASHIS  
LPLVFHYVLMVRFLVYTKTHV-AVTMSLTSMR-QHVIGLMLAITYLPTLVLRDSSFSQOK  
RSKPLRKHL SCHMVLPLYAKYSLTENCIFHGRLENLDHH-TETMSLLVTV-LKIVKYRLE  
STPLKKVTMVM L LCTEVL RHTS-MLVITLC-HLTL-CHLVHLL-CHKSTM-ELLACTQHS  
TSQMSFLAMLQIIKRSACKSTLH SKDHLVLRVILPSDLLSITHLLA-CIRHALMQLLMP  
YVKRH-NICP-INVESYLRVRA-SVLINSK-IQH-NSMFSAL-MHCQKQLLT L-SLMKS  
LWLLIMT-VLSMLDFVQNTTSILAILLNYQPPAHC-LKAH-NQNILIQCADL-KQ-VQTC  
SLELVAVVLLKLLTL-VL-FMTIS-KHTRISQLNASKCSTKVLLHMMFHLQSTD LK-AL-  
ENFLHAILLGEKLFLSHLIIHRTL-LQKS-DCLRLLIHRV LNM TMSYSHKLLKQHTLV  
MSTASMWLSQGQKLA FCA-CLIEIFMTNCNLQV-KYHVAMWLHYKQKM-LDFLRTVVRSL  
LVFILHRHLHTSALI-SSRLKDYVLTYQAYQRT-PTVDSSL-WVSK-ITKSMVTLICLSP  
AKKLFVTFVRGLALM-RAVMQLEMLWVLTYLSS-DFLQVLT--LYRLVMLTLKITQNSPE  
LMQNLHQVTS LNILYHSCIKACPGM-CVLR-YKCSVIH-KDCQTESC SSSFGRMALSLHQ-  
STLSRLDLKERVV CVTNVQLAFL LHQILMPAGIILWVLTMSITHL-LMFSSGALRVTRV  
TMTNIARYMEMHMLVVM LS-LDV-QSMSALLSALIGLLNTLL-EMN-GLILLA EKYNTW  
L-SLHCLLISFQFFMTLEIQRLSSVCLRLK-NGSSTMLSHVVTKLTK-RNSSILMLHITI  
NSLMVFVCFGIVTLIVTQPMQLCVGLTQESCQT-TYQAVMVVCM-ISMHSTLQLSIKVH  
LLI-SNCLSFTILIVLVSLMANK-CRILIMFHSNLLRVLHDAI-VVLFADTMQ MSTDSTW

MHII--FLDLAYGFTNNLILITCGIHLPGYRV-KMWLIMLLIKDTLMDTPAKHLPFSLI  
 MLFTQR-MVLMWRSCLKIRQHFLMLHLHSFGLSVTLNQCQRLRYSI IWVLISLLIL-SGTT  
 KEKPQHMYLQ-VSAQ-LTLPRLNLLRVLVLHLLSCLMVWVKDR-TFLETPVMVF--QKVQS  
 KV-HLQRDQHKLASMESH-LENQ-KHSLTTLRK-TALFNSCLKPTLLRAET-RILSPDHK  
 WKLTFFSSSLWMNSYSDISSRAMPSNTSFMEISVMDNLAVFI---A-PSAHKIHLN-RIL  
 SLWTAQ-KITS-QMRKQVHQNVCVL-LIFYLMTLSR--SHKICQ-FQKWSRLQLTMLKFH  
 SCFGVRMDMLKPSTQNYKQVERGNQVLRCLTCTRCKECFLKSVTFRIMVKMLLYQKE---  
 MSQSILNCVNT-IHLL-LYPTT-ELFTLVLALIKELHQVQLCSDNCGQLAHYLSIQILMT  
 SSPTHILL-LETVQQYIRLINGTLLLAICMTLGPNM-QKRMTLKKGFSLICVDL-SKN-P  
 WVVL-L-R-QSILGMLTFTSLWAISHGGQLLQOM-MHHRKH-F-LGLTILASRRNKLMAI  
 PCMLTTFSGGTQILSSCLPIHSLT-ANFLN-EELL-CLLRRIKSMI-FILFWKKVGLSL  
 EKTTELWFQVIFLLTTKRTCLFSYFLLSLVVVTLTGAPLLMMFKLLITLNLHL-GGFT  
 ILMKFELDQTLFI-LRIYFFHCFILMLQGFIILLIRLATLSYLLRMVFIILLPQRNQMSLVG  
 FLVLP-TTSHSR-LLLTILLMLLYEHVTLNVCVTTLSLLFLNPWVHRHIL-YSIMHLIALS  
 STYLMFPRLMFQKSQVILNTYESLCLKIKMGFSMFIRAINL-M-FVIYLLVLT-LNFLS  
 CLLVLTQLILEPFLQPFLHLLKTFGARQLQPILLAI-SQLHLCSSMMKMVQSQMLLIVLKI  
 HLLNSNALLRALRLTKEFTRPLISGLFPQEML-DSLILQTCVLLERFLMLLNSLLSMHGR  
 EKKFLIVLLITLCSTTQHFFQPLSAMAFPLS-MIFASPMQMILL-SREMM-DK-RQDK  
 LVLLIIIIINCMISWVVSLLGILGTMLLQLVIIIIINIGILDMASLGPLRETYLMCLSP  
 LMANLAPHLLLIIVIGH-MIMVFTPLLALATNLTTEL-YFLLNF-MHRPRFVDQNYPLTLR  
 TSVSILILMDSLVLVC-LLLQRDFNHFNFLAVMFLISLIPFEILKHLKY-TFHLALLGV-  
 V-LHLEQMLHLKLLFYIKMLTALMFLOQFMQINSHQLGAYILLETMYSRLKQAVL-ELSM  
 STLLMSATFLELAFVLVTIQFLYVVLAKNLLWLILCL-VLIVQLLTITPLLYLLTFQ  
 LALLQK-CLFLWLKPP-IVICTSAEILLNVLICFSNMVAFAHN-IVHSQVLLLNRIATHV  
 KCSLKSNNKTFPQL-NILVLI FHKYYLTL-SQLRGLLRTCSLIR-HSLMLAS-SNMAN  
 A-VILMLEISTFVRSSMDQCCCHLCSLMI-LLPTLLL-LVVLPLLDGHLVALLFKYLLL  
 CKWHIGSMALPLPKMFMSMRTKNKSPNTLRLRVKFNHLQQHQLHWASCKTLTRMLKH-  
 THLLNNLALILVQFQVC-MISFRDLIKSRRRYKLTG-LQADFKAFKPM-HNN-SGLLKS  
 GLLLILLLLKCLSVFLDNQKELTFVERATTLCPSHKQPRMVLSSYSMRMCHPRRGTS  
 PQRQ QFVMKAKHTSLVKVFLCLMALLGLLHRGTSFLHK-LLQTIHLSQEIVMSLLASLT  
 TQFMI LCNLSLTHSKKSWTSTSKI IHHQMLILATFQALTLLSSTFKKKLTASMRSLKI-  
 MNHSLT FKNWENMSNINLGLGMFGSASLLD-LPSSWLQSCFVA-LVVAVASRVHALV  
 VLAASLMRM TLSQFSRVSNYITHKRTYGFVYEIFYSWINYCTASKN-QCFSCKYCSCY  
 SNDTATSLTPF RMACYWRCISCCFSERYQNNCAQ-KMAASPL-GLPVHLQFTA  
 AICYHLFTSFACRCRYGG AIFVPLCLDIFSTMHQRM-NYYEMLALLEVQIQEPITL-  
 CQLLCLLAHT-L-LLYTI-QC HRYNCRY-R-RHFNTKTQRRLPNWWLF-G-ALRC-  
 RLCRCTWLFHRSLLPA-VYTNYYRH WY-KCYILHL-QAC-RPTECANTHNRR  
 LFRSC-SSNGSNL--ADDDY-RAFVSTRK-VRT YVLIRFGRNRYVNS--RTSFCF  
 RGILASHTSHPYCASIVCVLLQYC-REFSKTNGRLRL AC-KSELF-RSS-SSGLNE  
 LTIIILFGLTLLIMADNGTITVEELKQLEQWNLVIGFL FLAWIMLLQFAYSNNR  
 NRLFYIIKLVLFWLLWPVTLACFVLAAYRINWVTGGIAIAMACI VGLMWLSYFV  
 ASFRLFARTRSMWSFNPETNILLNVPLRGTIIVTRPLMESELVIGAVIIRG HLR  
 MAGHSLGRCDIKDLPKEITVATSRTL SYYKLGASQRVGTDSGFAAYNRYRIGNYK  
 LNTDHAGSNDNIALLVQ-VTTDVSSC-LPGYNSRDIDYHYEDFQDCYLES-RYNKFN  
 SETII-ASN-EELFGVR--RTYGVRLSIKRT-KLFSS-H-LYLHLASYITIRSVLEVR  
 LYY-KNL AHQEHTRAHHFTLLLTINLH-LALAHTLLLLLVLTVDIPISCVQDQFHQ  
 NFSSDKRRFN KSSTRHFFSLLL-YF-YFASPLRERQNE-AHFN-LLFVLFSLSAI  
 PCFNNAYYILVFTR NPGSRRTLYQSLNEHETSHCFDLYFSMQLHMCSTALCI--TSCA-  
 RSL-GTTLGVLILIA LLGFVL-ERFYLFIDGTLWFKHAHMLLSTVKIQLVVRL-LG  
 VGTFMKVTKLLHLETYLL F-INEQIKMSDNGPQSNQRSAPRITFGGPTDSTDNNQ  
 NGGRNGARPKQRRPQGLPNNTAS WFTALTQHGKEELRFPRGQGVPIINTNSGPD  
 DQIGYYRRATRVRGGDGKMKELSPRWYFY YLGTGPEASLPYGANKEGIVWVATE  
 GALNTPKDHIGTRNPNNNAATVLQLPQGTTL PKGF YAEGSRGGSQASSRSSRSR  
 GSNRSTPGSSRGNSPARMASGGGETALLLLDRNLQLE SKVSGKGQQQQGTQVTKK  
 SAAEASKPKPKRTATKQYNVTQAFGRGPEQTQGNFGDQDL IRQGTGDKHWPQIAQ  
 FAPSASAFFGMSRIGMEVTPSGTWLTYHGAIKLDDKDPQFKDNVI LLNKHIDAYK  
 TFPPTPEPKKDKKKKTDEAQPLPOROKKOPTVTL LPAADMDDFSROLNSM

SGASADSTQA-TLMMTTQGRWAM-TFSQFRLRYIVYSCAE-ILVTKQHK-V-LTLISHSN  
L-SMCNIREDLKEPPHFHRGHAHEYDRGYSE-C-GELPIWKSPNV-N-F-CYPHVILIAS

**FIGURE 24**

TQEKPTNLDLL-ICSLNEL-NLCSRSAACLVHLRSINNNKFYCR-QETSNSSLFCRLLT  
 VSSVLQSIISIPRFRPGVTER-DGEPCSWCQRENTPTQFACPSG-RRASAWLRGLCGRG  
 PIGGT-TPQKWLWSSRAGKRRTAPA-TALCVH-TF-CLKHQSRPQGR-AGCRNGRHSVR  
 S-RYNTGSTRATCGRNPNCIPQCSSS-ER--GSRWS-LWHRSKVL-LR-RAWH-SH-RL-  
 TKLEH-AWQWCTP-THS-AQWRCSHSLCRQQFLWPRWVPS-LHQRFSTRGQVNVHSFRT  
 T-LHRVEERCLLLP-P-A-NCLVH-AL--ELRAPDTLRN-ECQEI-HFQRGMPKVCVSS-  
 LKSQSHSTTC-KEKD-GFHGAYTLCVPCCISTGV-QYALVYLDDEM-SLR-SFMADVRLSE  
 SHL-TLWH-KFSY-RTYYMWVPTY-CCSENAMSCLSRPRDWT-A-CCRLSQPLKH-NSTP  
 QGR-D-MFWRLCVCLCWLL--ACLLGSSC-C-YWLRPYWHYW-QCGDLE-GSP-DTES-T  
 C-H-HCWRFSFE-RGCHHFGIFLCFYKCLY-HYKES-LQVFQNH-C-VLR-L-SYQGKARK  
 RCLEHWTTEISFNNTTVWFSLTGCWCYQINFCAHT-CSKPLNS-FAKSSCHHT-WYF-TVI  
 TSCRRHGLYFRPAHQQCHYYGICNWWSCCTTDFSVVV-SFGHYC-KTQAYL-MD-GET-CR  
 S-ISQGLGDSQISHYRCF-HRQGSNTGCFR-HQGLCKMLH-CC-QGTRNVH-SSHWR  
 KVAITQLR-SLHRSKQGTLPSTVYTQGAATTHAS-GTKRSNLS-R-FT-HSTYL-GGCS  
 QER-TRSTRDAR--LHKWSYRRHTSLCKWPHALRD-GQRTILRIVSWFTGYKQCLSLKRG  
 CTN-RCNLWRRYCLGSSRLQECENHI-A--TC-QSA--KVLCLHC-IRYRSY-VCMCCSR  
 GCCEDFTTSF-SPYQHGY-S--VECSYILLI--CW-RKLFITYVLFLLPSR-GRRGRCRV  
 -GRRN--NL-T-VRYRG-LSRSPSGIWCLS-NSSS-GRRRGRLAG-YY-AIRD-ARTRTY  
 T-RTS-SVYWLFKTY-QCCH-MC-HR-GGTKC-SYGDCKCC-HTPETWWWCSTRCTQQGNQ  
 WCHAKGE--LH-AKWPSYSRRVLFAPWT-SC-EVSACCWT-PKCR-GHPAS-GSI-KFQF  
 TGHILTCTIVSRHIWC-TTSVFTSVRADGSYTGLYCSQ-QSSL-AGCHGLS--PEA-SGS  
 T-TRGATKHRRFQN-GEICRTEACRCEAKN-GLH--GYHNTGRN-VSYQ-VTLVC-YQW-  
 ALP-FSEHA-R-RYVFP-EGCTLHGR-CYH-W-YHLCNTLQKGWWHY-DALKSFEEAS  
 --VYNHVPWTRMCWLYT-GS-DCS-EMQICILCTTFRST-C-GRDSRNCILEFERNACSC  
 -RDKKINAYMHGC-SHNGNHPT-V-RN-NSRGHR-LWCPILLY--RACSFYYEAEISK  
 -AACHNANWLCDTWF-S-RGCALYAFS-SSCRSVSIITRCCYII-WIPHFVIKDI-GALC  
 RNSFFGWLRLQRLVLFRTAYRVC-IS-AW-QNCVPHSGEPRRVSS-R-GSFT-QTKESLI  
 PAGG-DYKSVHNCQGH-SPHTACGYVYDIWTAVSNSILGWC-CYKN-TSCKS-G-DFLCT  
 T---HTT--SFRVLPYS--EFSW-VHVCFKPHKEMEISSSWWFNFN-MG--QLLFV-CFI  
 STSTA-SQIQCTSTSRGLL-SPCW-CC-LLCTHTRLQ--NCWRAW-CQRNYDPSSTAC-F  
 GICKASS-CGV-TLWSENYYLNGCRSCDVYGYSL--S-DRCFHSMCVWS-CYTISSTTR  
 VFFCYDVCTTC-V-ITARYILMCE-VHW-LSVWSLHSYNC-GDPLSY-RSSPYKDVRVQR  
 TSD-CFLQGNILHYNHQACVV-TRWSYLHRD-TKIGWVL-KG-CLLYRAAYRPCTNSTIT  
 KCEF--FQTHMF-HKIC--FKSNDRLHKASFTRAICHILPRLEWRCSGY-L-TLFSEFQE  
 RC-ITA-ANCLAH-PGYNQDNVQTKHLVFTLSLEYKASRYFKFI-SSGSRHTRNGQSCL  
 -KSTTHL-RSSGKSYHTEGSHRV-RENYRSCRQCHT-TIR-RC-SNTRVRS-GSYGCLCG  
 KHKHYH-ET--AFTSLRFKNNCHSWYCCN--CSLE-NFGLCQTLIRTSSNYNIKLR-EIS  
 TTCV-QLYALCVYIIIVPIVYFY-KYQF-N-SFTTYNYC-K-C-ECC-IMFGCRH-LCEVT  
 QIF-IVHNRYVAIVVKYLLRFSNLCNCCFWCTLI-FWCSFLL-WR-RIVS-FV-RYYYGF  
 L-RFFSLQHLFKWIRLP-FLSSS-NHSGDDFIVQARLDNFRSGR-VGFGIYVVKILLFI  
 RSFSYNAGVLWLF-C-SFHQQFLAHVVYH-YCTNGTRFCNG-DVHLLCFFLLHMEELCSYH  
 GWLHLFDLHDVL-AQSCHTR-VYNYC-WHEEIFLCLCKWRPWLLQDSQLELSQL-HILHW  
 -YIH---SCS-FVTPV-KTNQPY-PVIVYC--CCCEKWRASPLL-QGWSKDL-ETSALPF  
 CQFRQFES-QH-RFTAY-CHSF-WQVQMRRVCF-VCFCVLQSAADVPTYSA-PSSCIRR  
 R-Y-SFR-DV-CLCRHLFSNF-CSYGKT-GTCCYSSQRVSKGCSFRWCFFYIRVSCPTRC  
 C-YRC-HKGCY-MSQTFTSL-LRSDR-QL-QFAHL--G-KHDAQRSWRMY-L-CKAYQC  
 PSSKKSQCFTHLECKRLHVFI-TAA-TNS-CCQEEQHTF-TNLCYN-TGCQCHNY-NLTQ  
 GW-DC-YLF-TYA-GHIIVRSCCIGLLYRYASTYIVNP-WLHK-NHWLQSHSGWCHS-HH  
 FY--LFCK-TCWF-RMV-PAWWFIQK-QKLPCSSCYHYKRDWFHSAWLTGYCAESNQW-L  
 LAFSTSCF-CCWQHLLHTFQTH-V--FCYLCLRSCC-VYNF-GCYGQTCAILL-H-FARG  
 FYFL--ASSRHSLCAYGWFHHTVS-HLPGGFC-SSNNF-C-VL-TWYMRKVRSRYPYQ  
 W-MGS---ALQSSIRSFLWC-CDESHS-HLYSSCATCGCFRCVCFSSGWYCHIGDLCC  
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ILGSPSMVCHVFSYCAFLDNSNLCILYFSEALPLVL-QLS-EKSHV-WSYI-YLRGGCFV  
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VS--IHHYFE-L-PCGNEVQL-TFDTRSC-HIGTSFCSNRNCRRLRYVCCFERAAAEWYEW  
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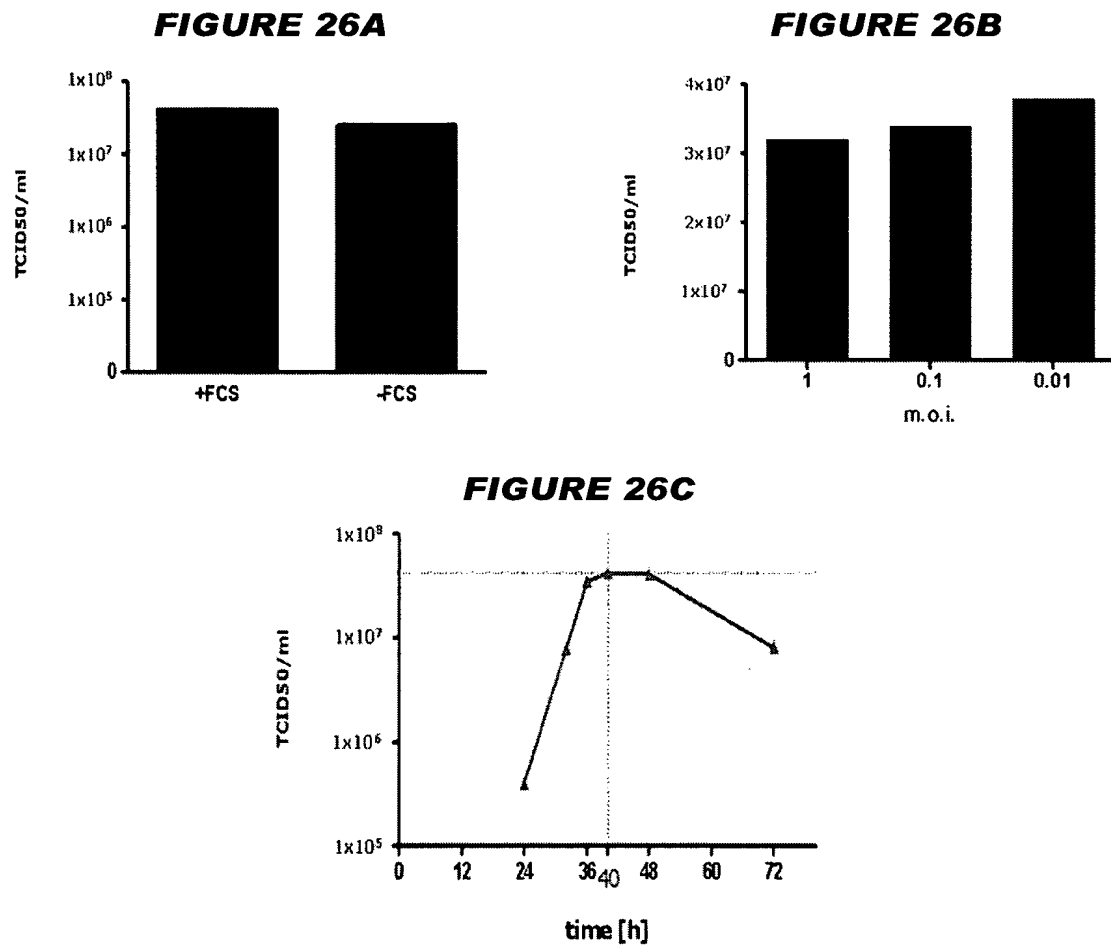
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**FIGURE 25**

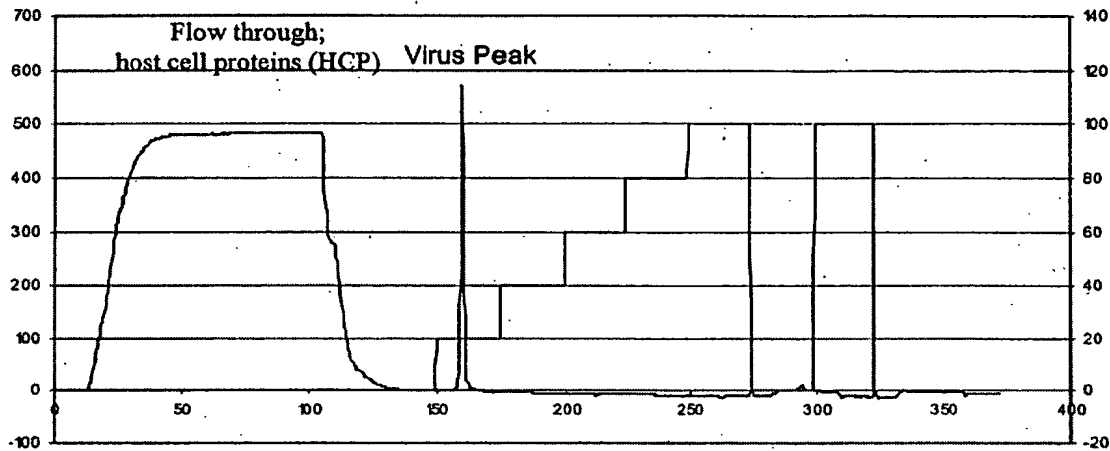
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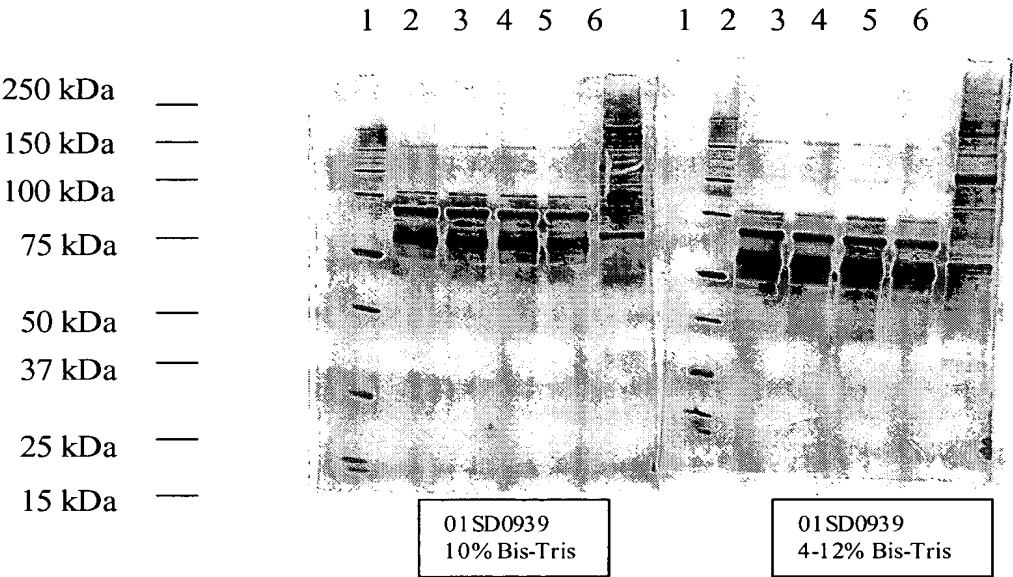
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**FIGURE 26**

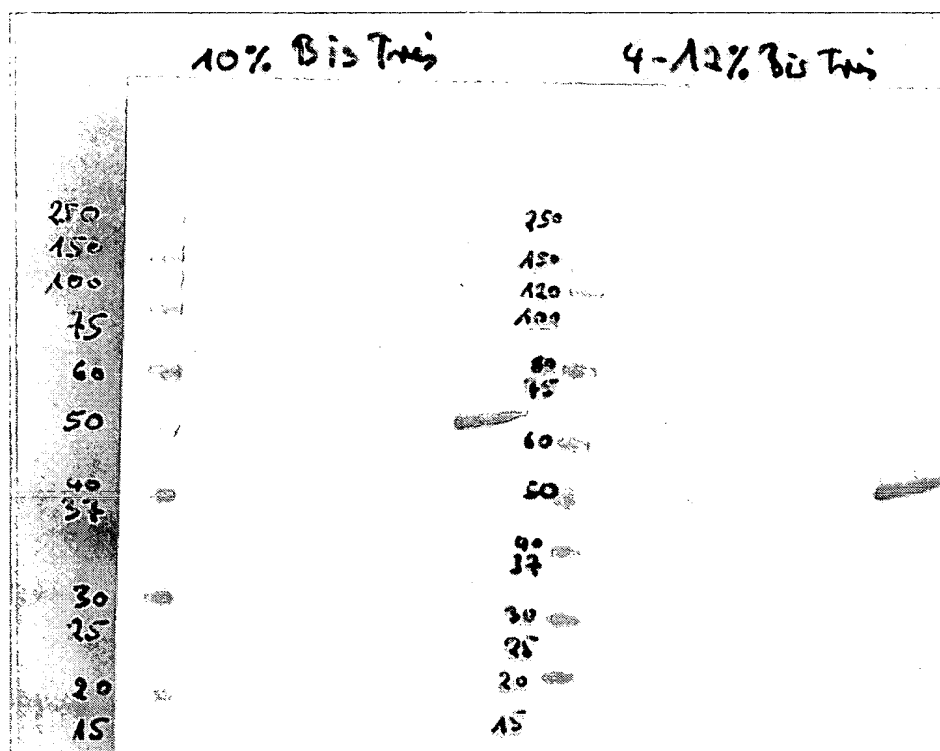
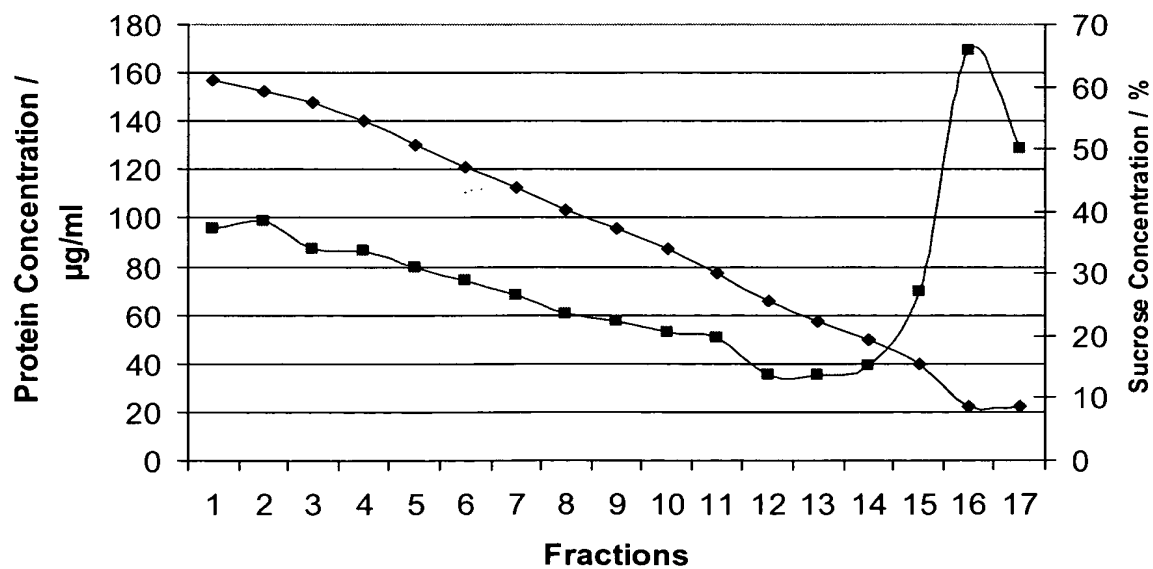
**FIGURE 27**



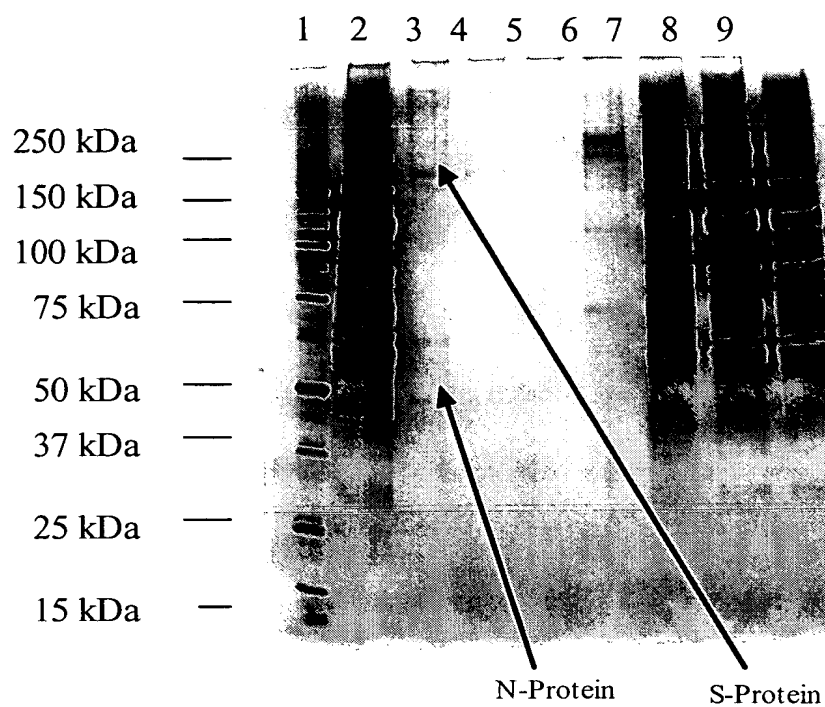
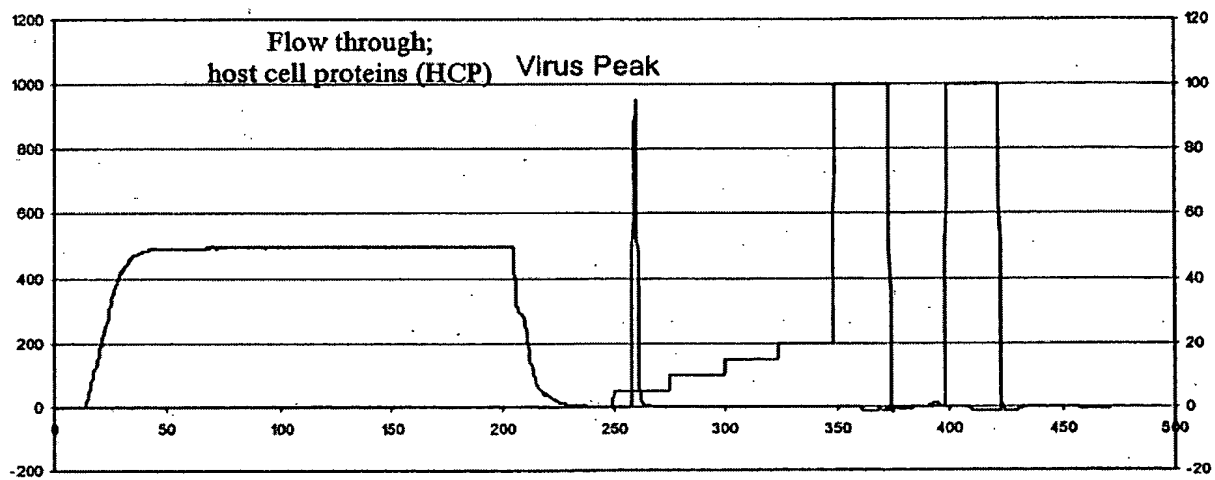
**FIGURE 28**



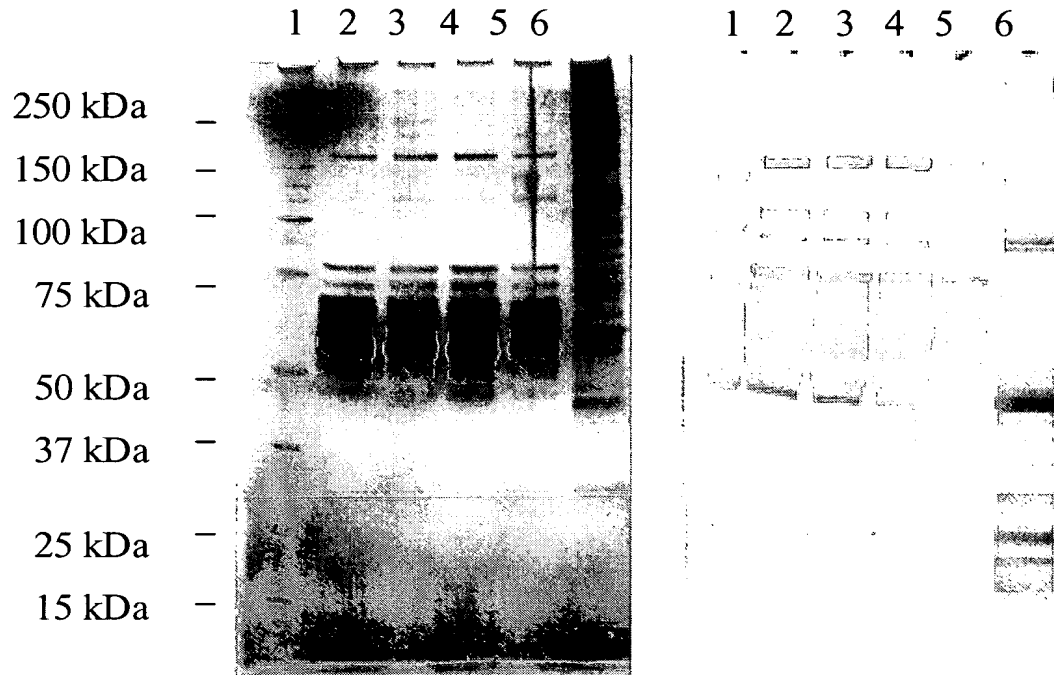
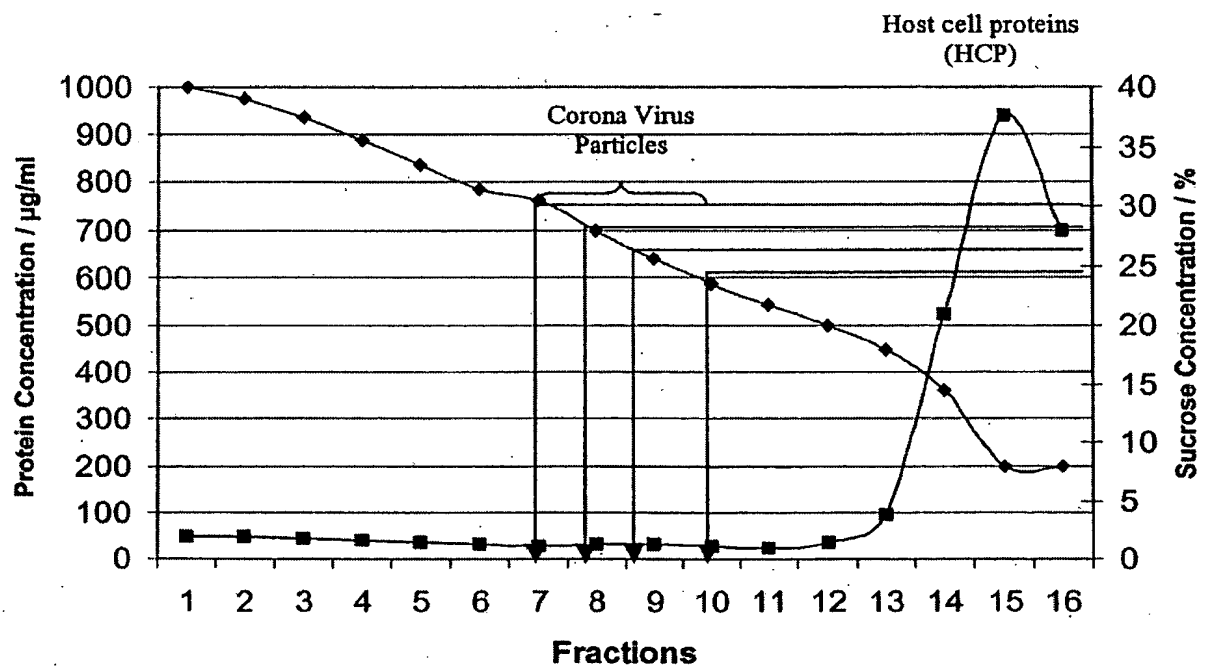
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**FIGURE 29****FIGURE 30**

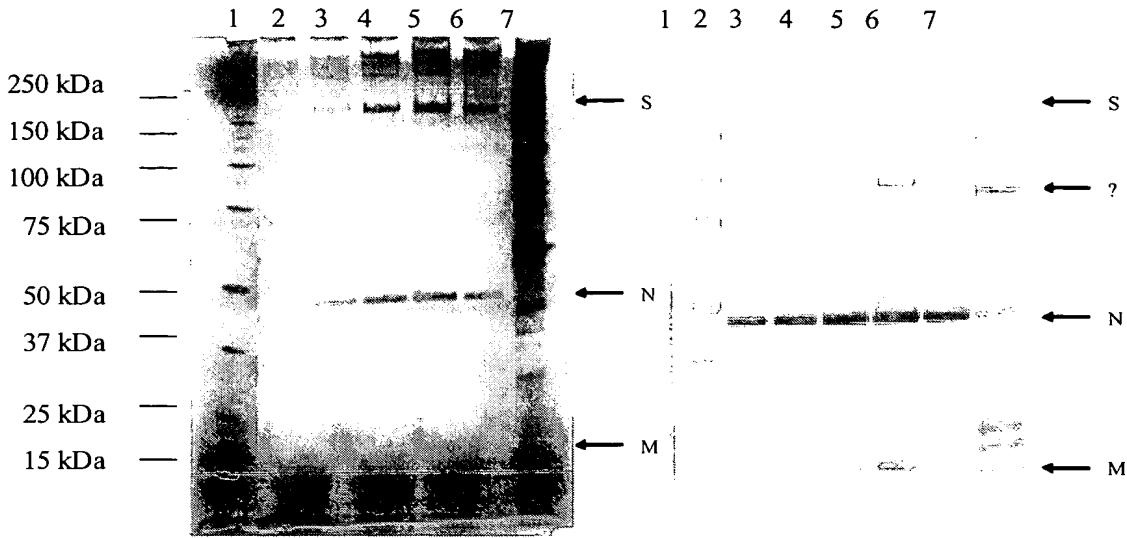
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**FIGURE 31****FIGURE 32**

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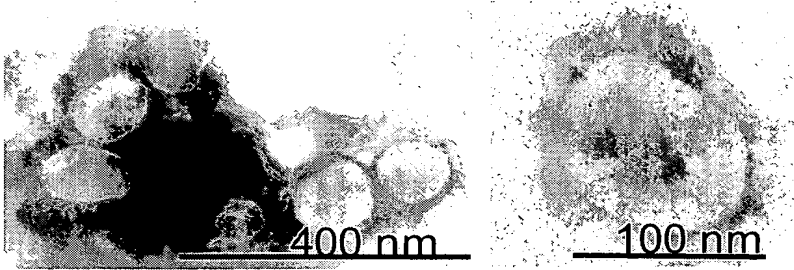
**FIGURE 33****FIGURE 34**

**FIGURE 35**

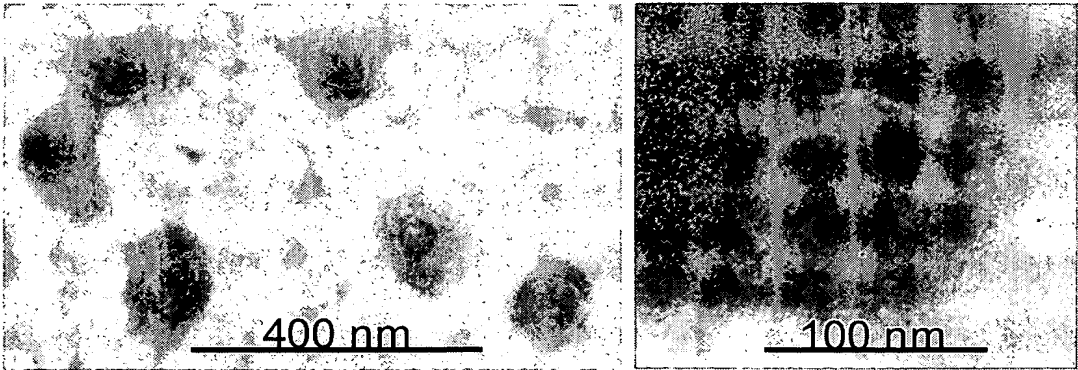


**FIGURE 36**

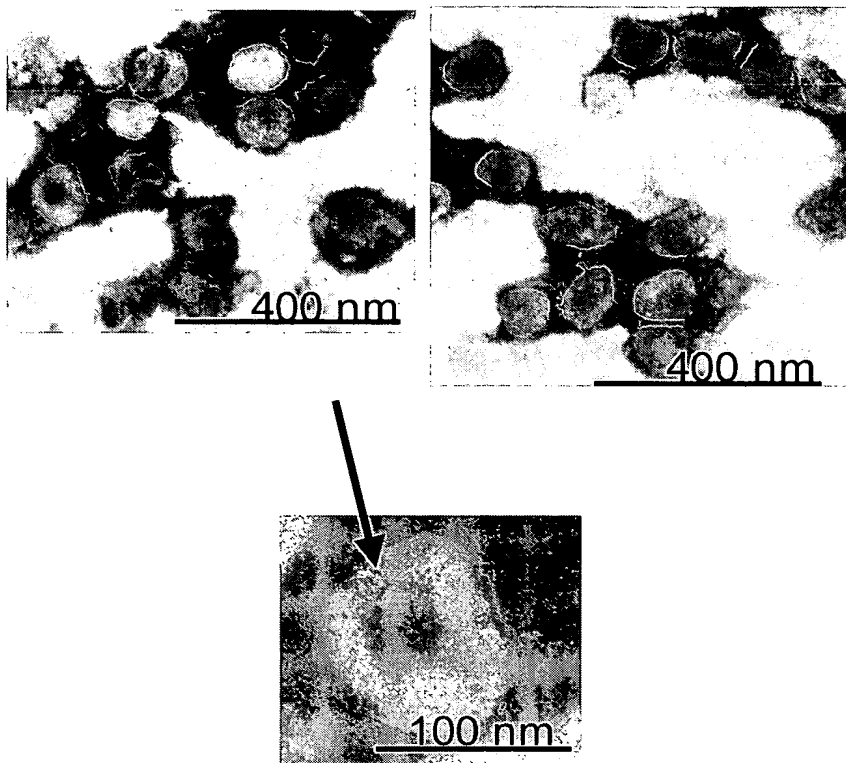
**FIGURE 36A**



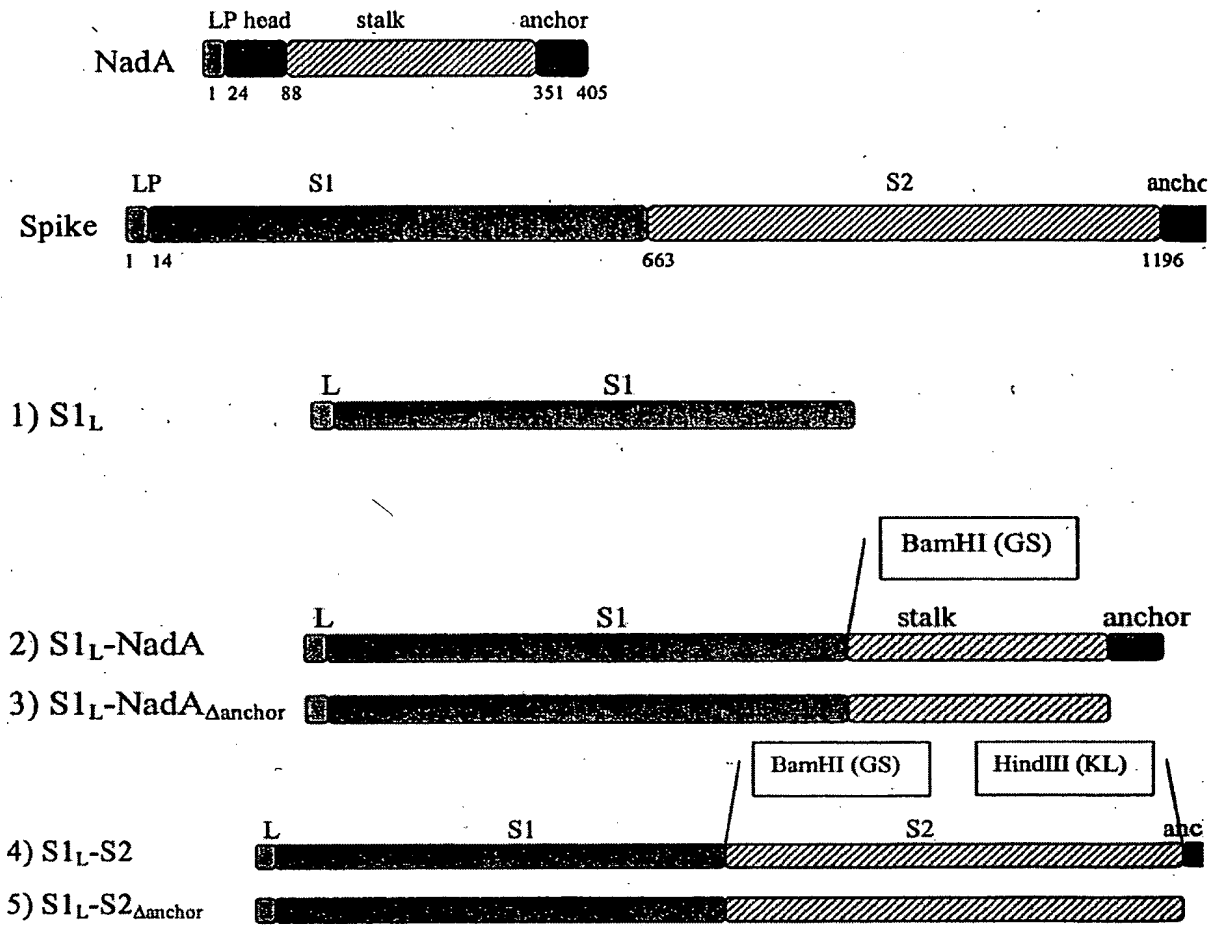
**FIGURE 36B**



**FIGURE 36C**

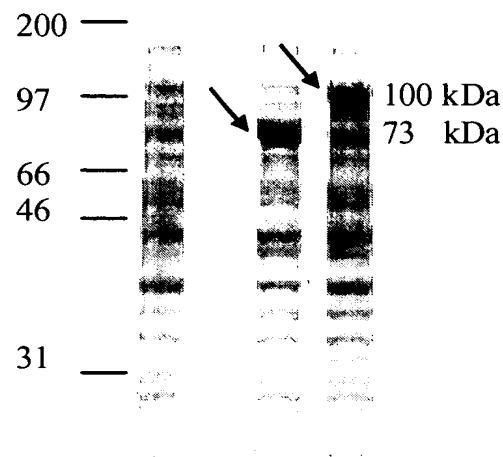


**FIGURE 37**



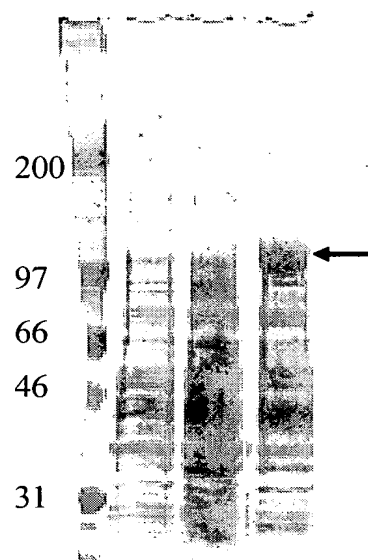


**FIGURE 38**

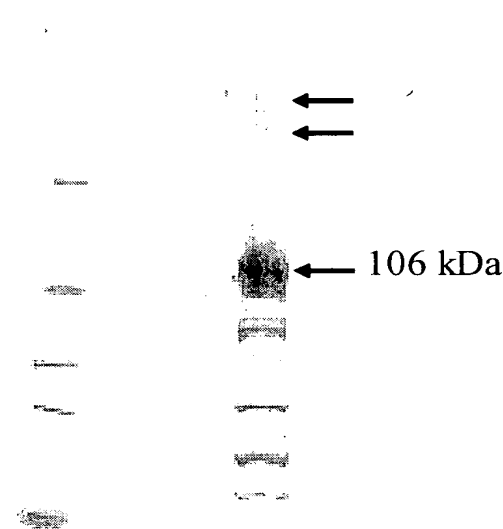


**FIGURE 39**

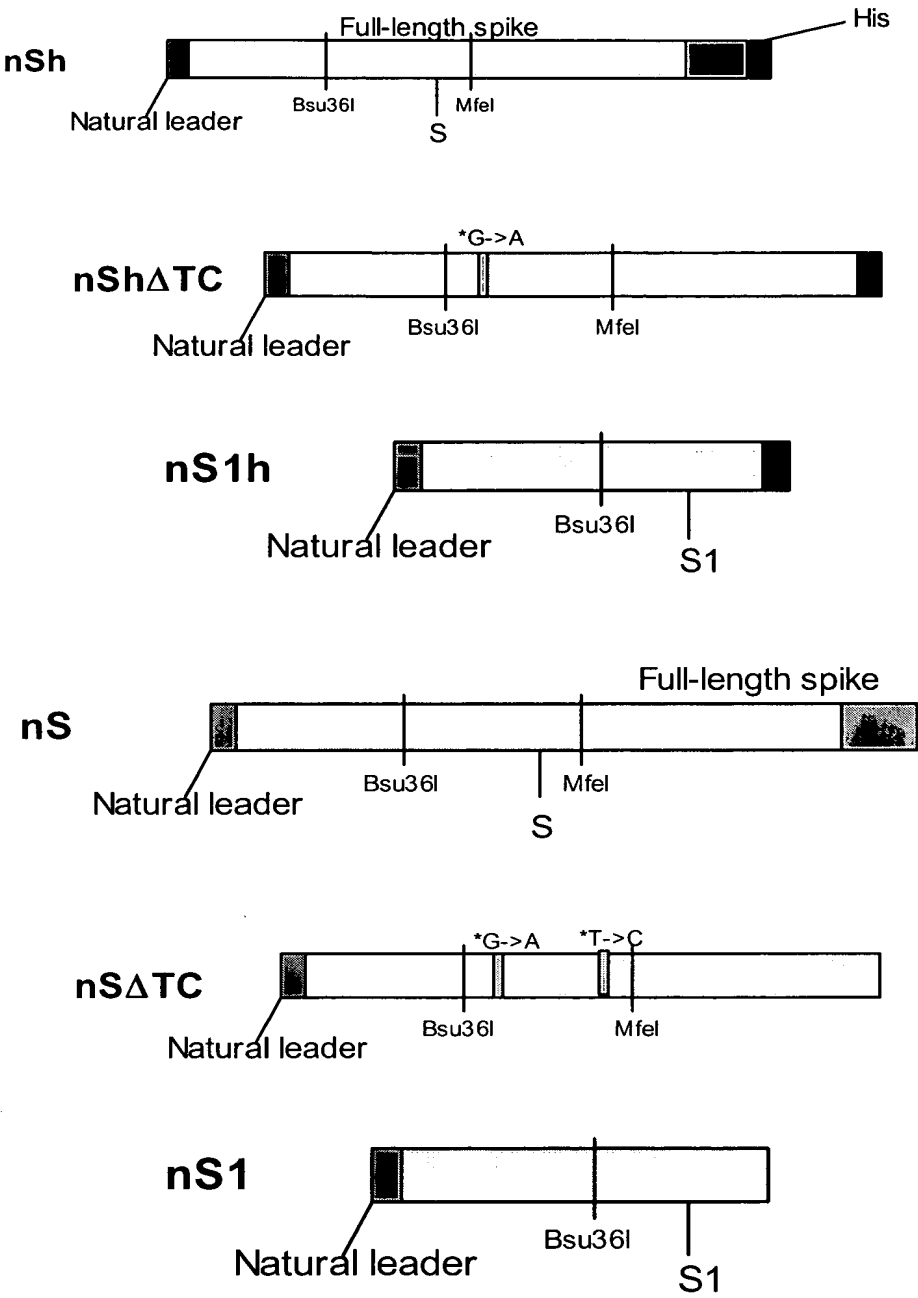
**FIGURE 39A**



**FIGURE 39B**

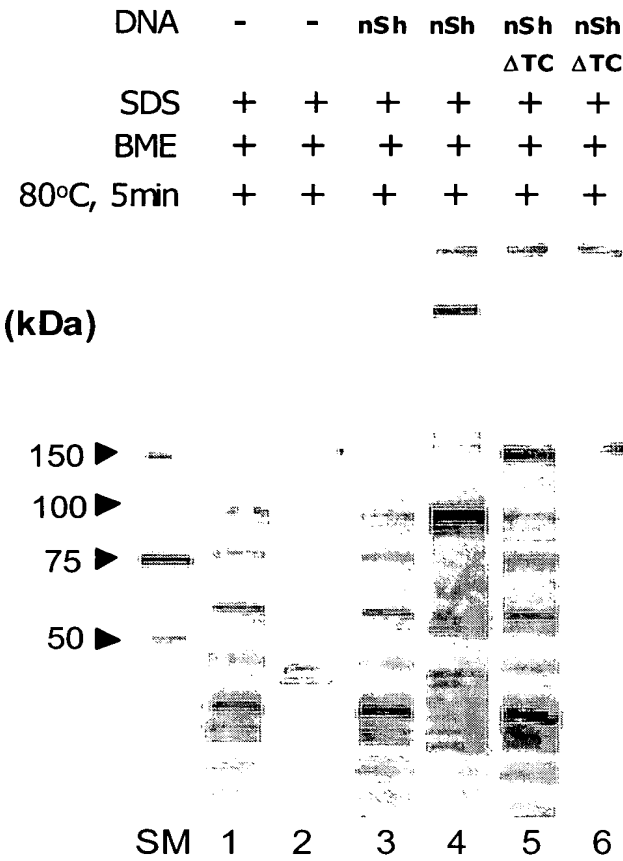


**FIGURE 40**

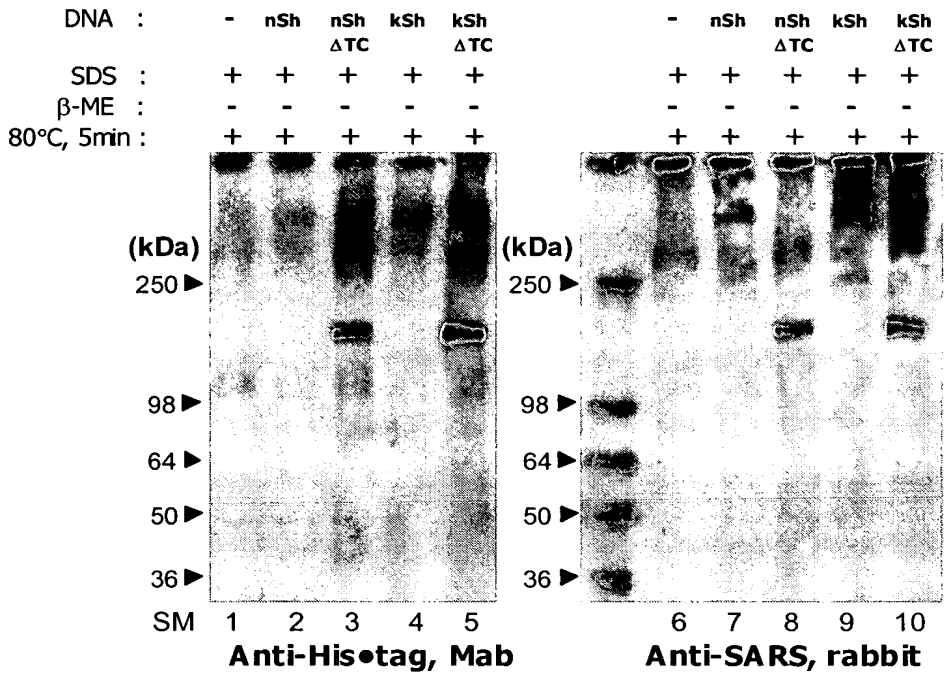




**FIGURE 43**



**FIGURE 44**



**FIGURE 45**

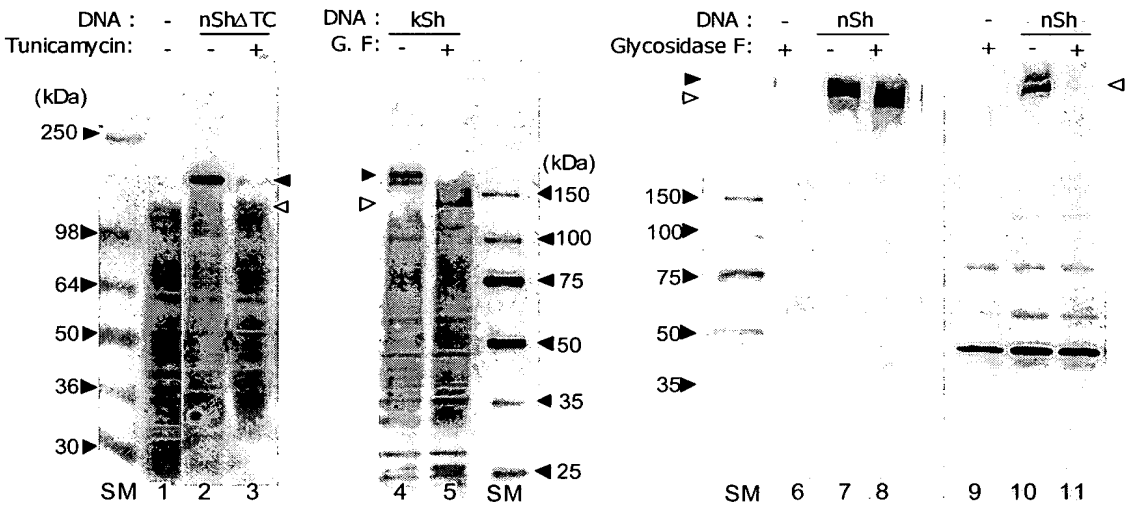


FIGURE 46

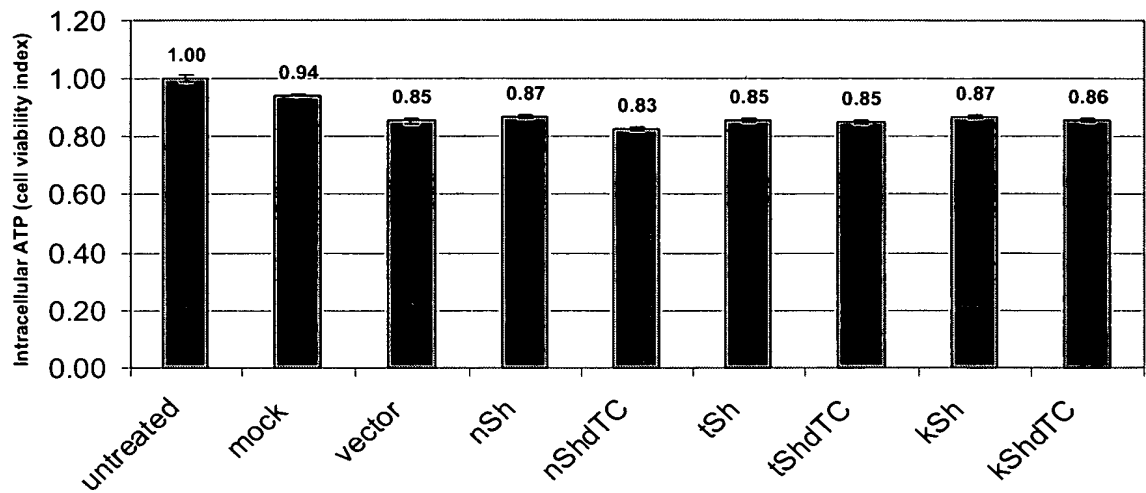
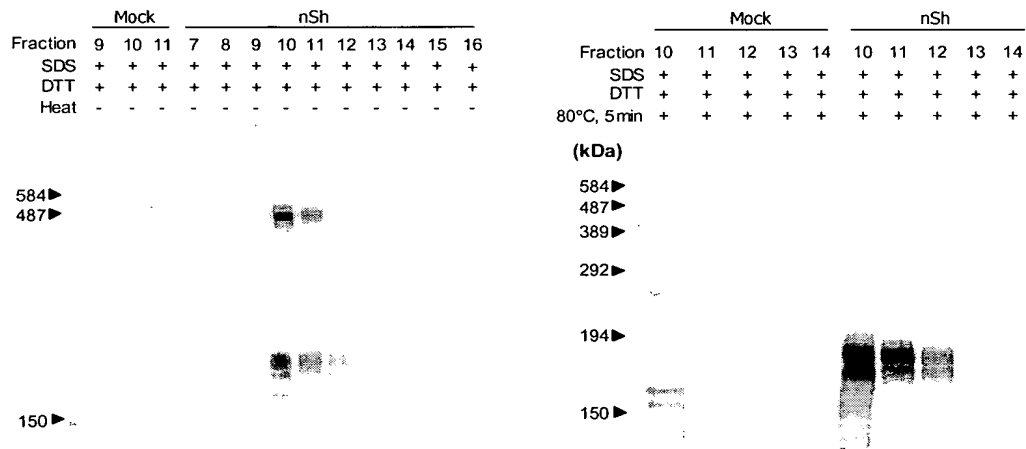
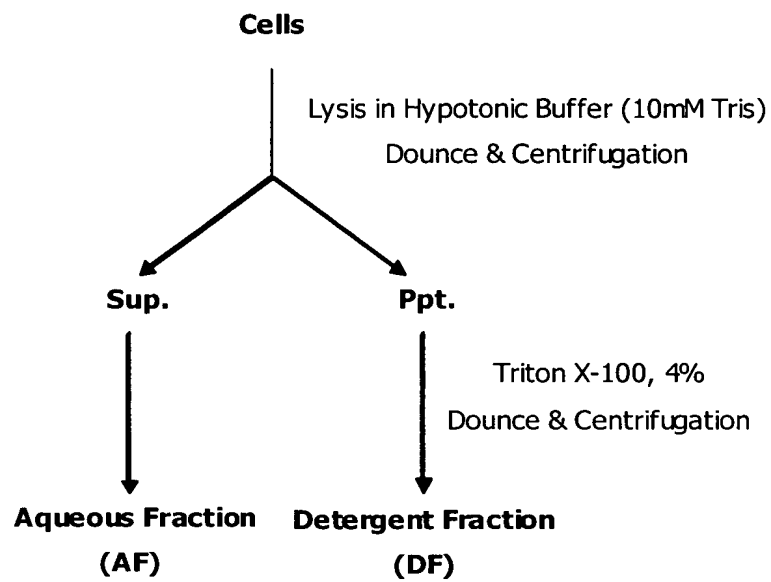
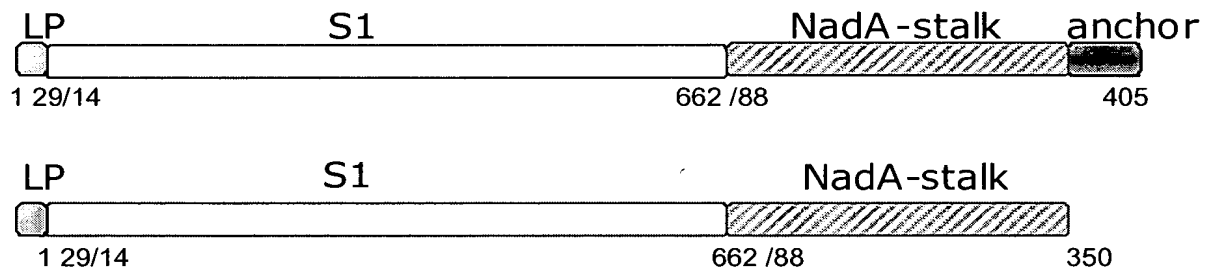
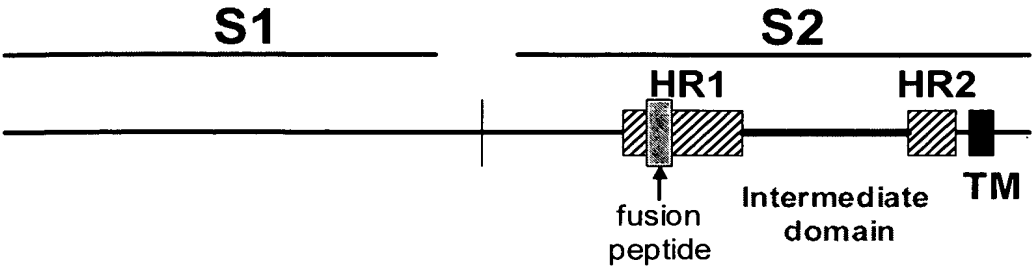


FIGURE 47



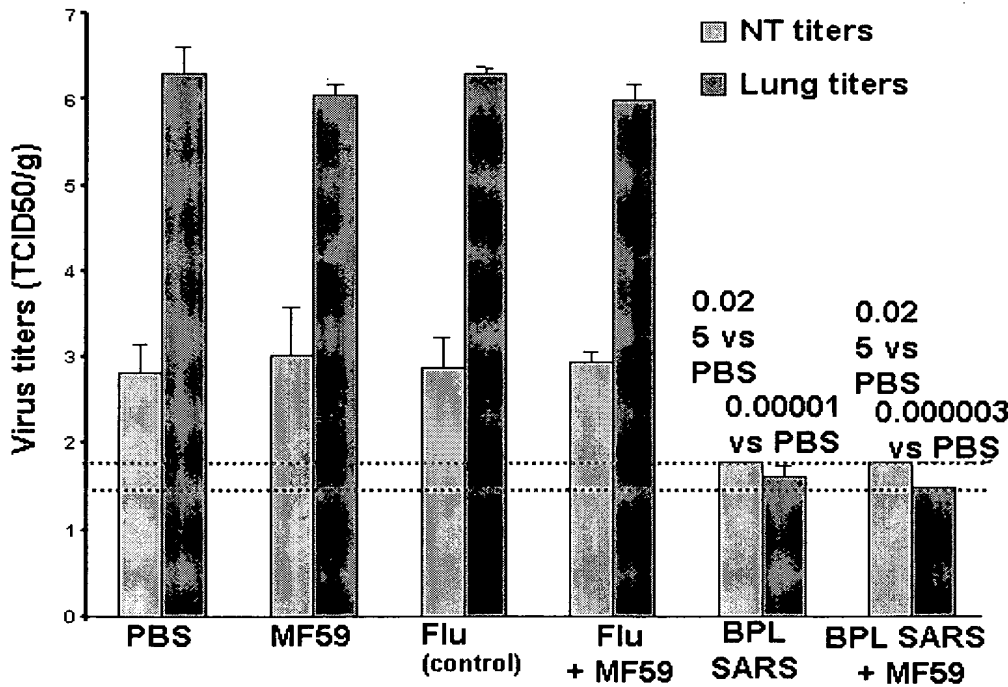
**FIGURE 48****FIGURE 49**

**FIGURE 50**



- a) Leader(NadA)-HR1-GGGGGG-HR2-GGGGSG-stalk(NadA)-anchor(NadA)
- b) Leader(NadA)-HR1-GGGGGG-HR2-GGGGSG-stalk(NadA)
- c) Leader(NadA)-HR1-intermediate-domain-HR2-GGGGSG-stalk(NadA)-anchor(NadA)
- d) Leader(NadA)-HR1-intermediate-domain-HR2- GGGGSG-stalk(NadA)
- e) HR1-intermediate-domain-HR2- GGGGSG-stalk(NadA) - HHHHHH
- f) Leader(NadA)-HR1-intermediate-domain-HR2-anchor(NadA)
- g) Leader(NadA)-HR1-intermediate-domain-HR2

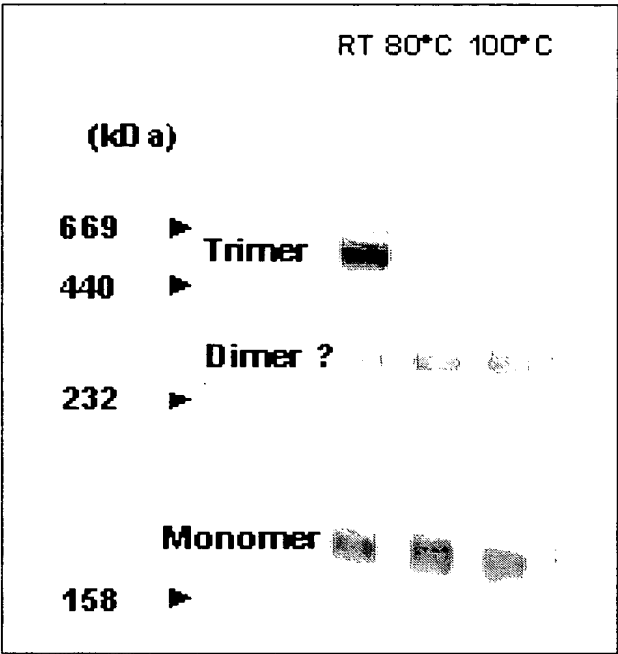
**FIGURE 51**





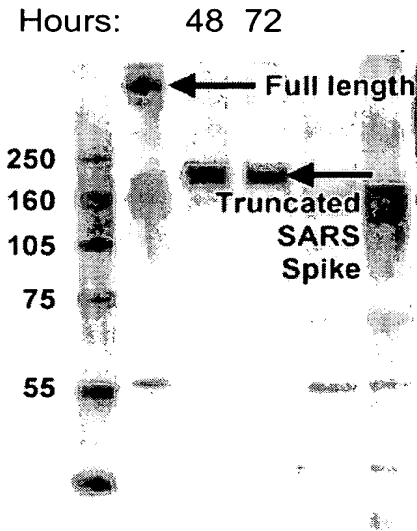


**FIGURE 54**

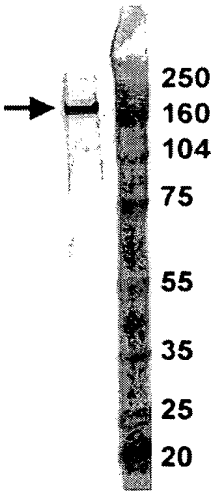


**FIGURE 56**

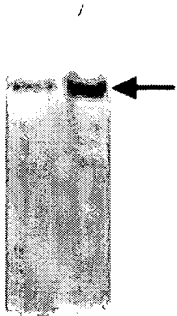
**FIGURE 56A**



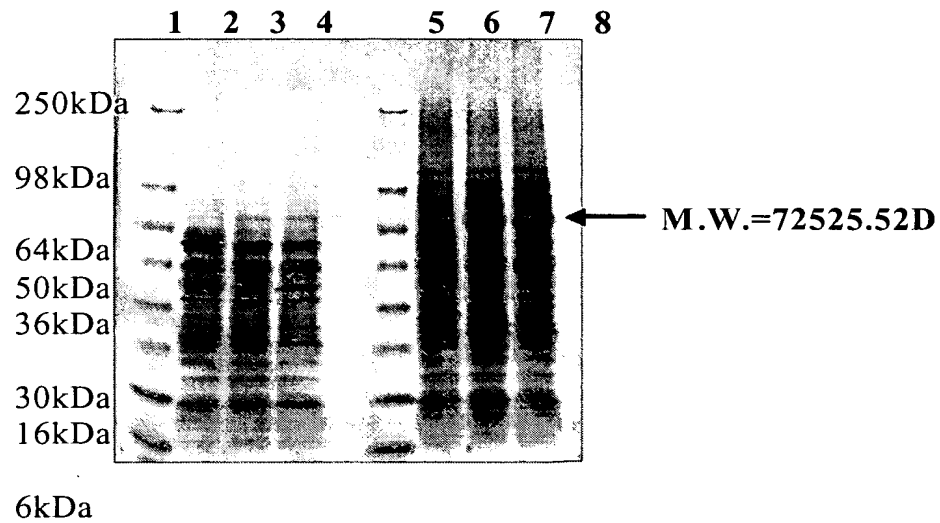
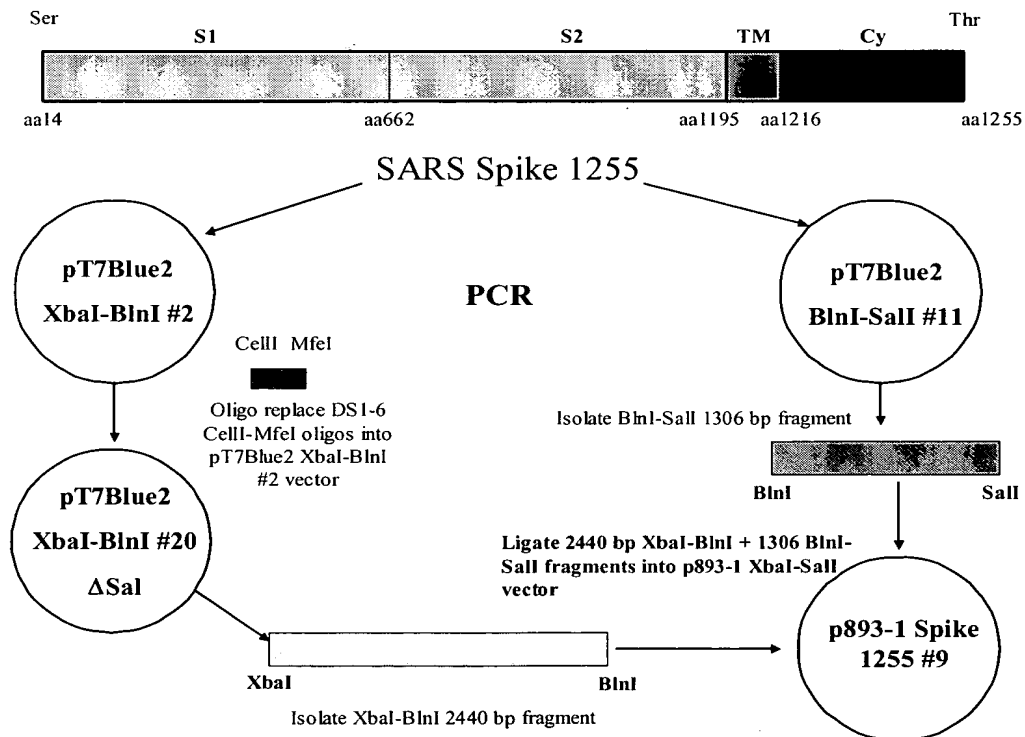
**FIGURE 56B**



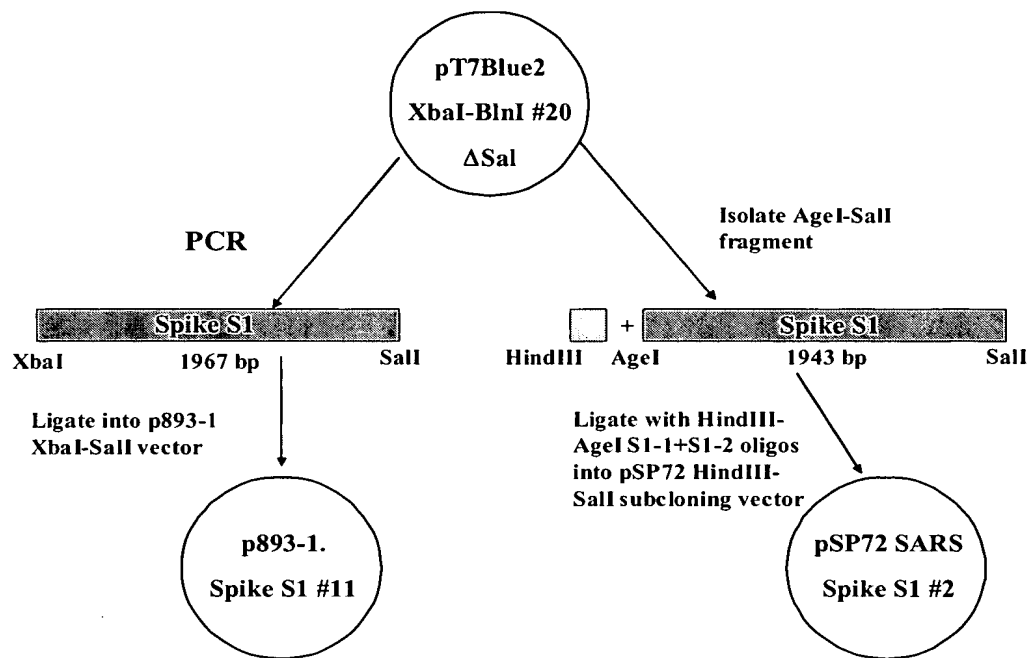
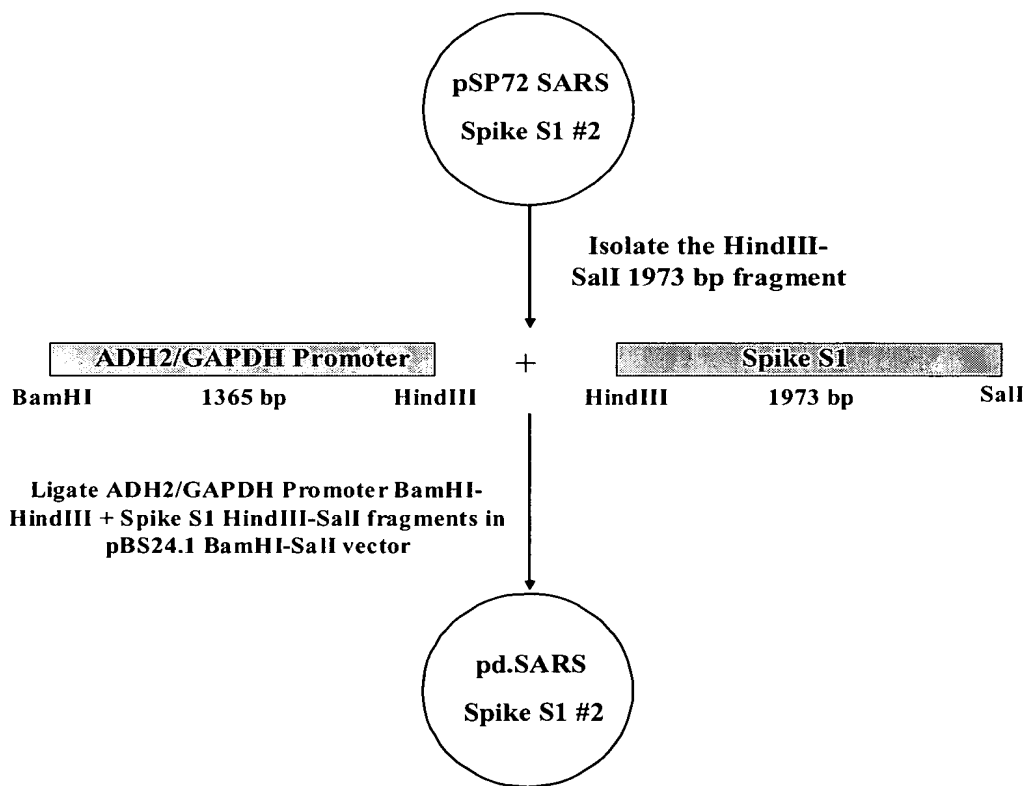
**FIGURE 56C**



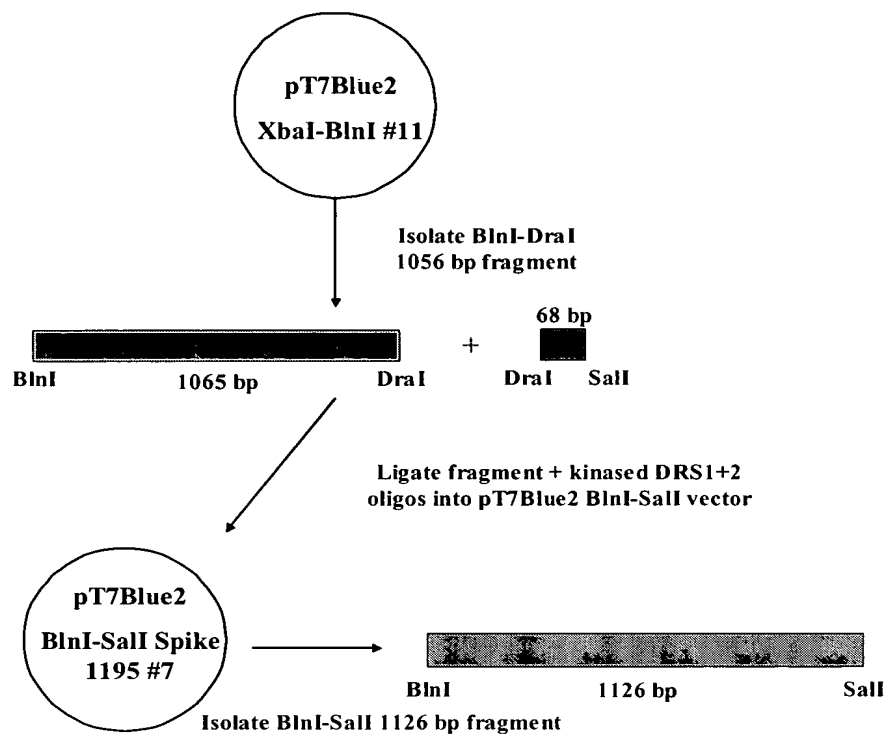
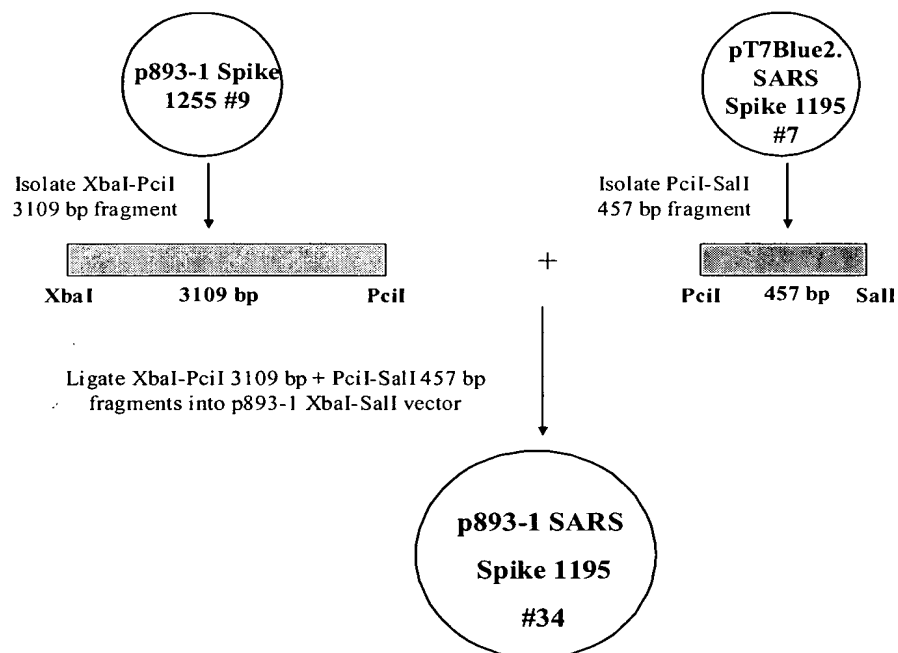
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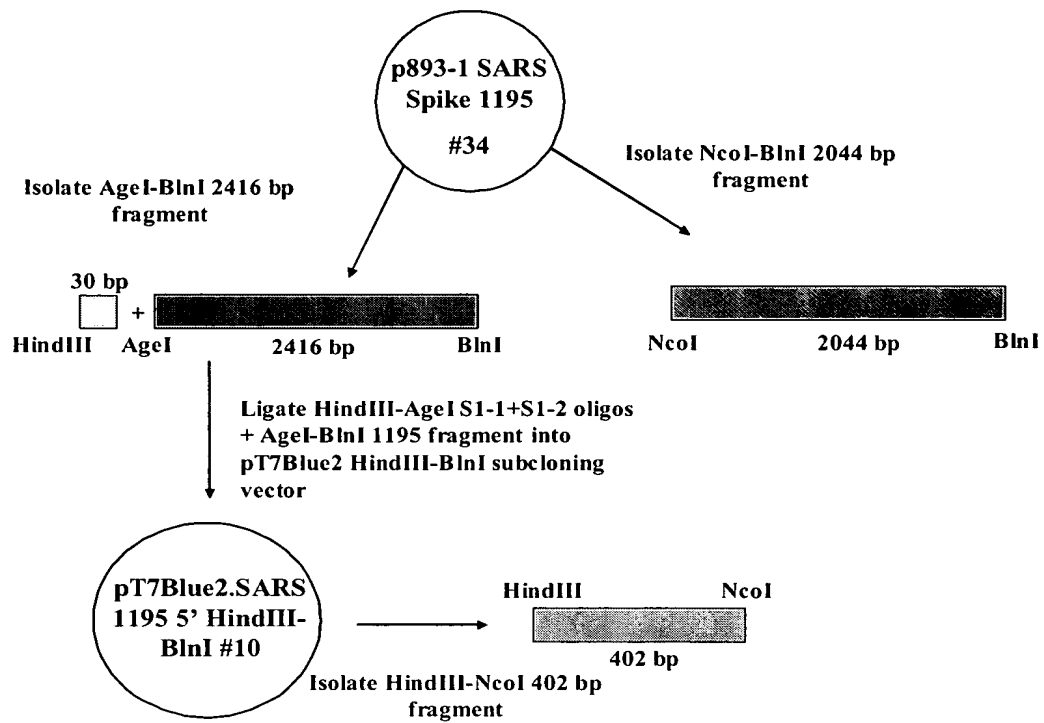
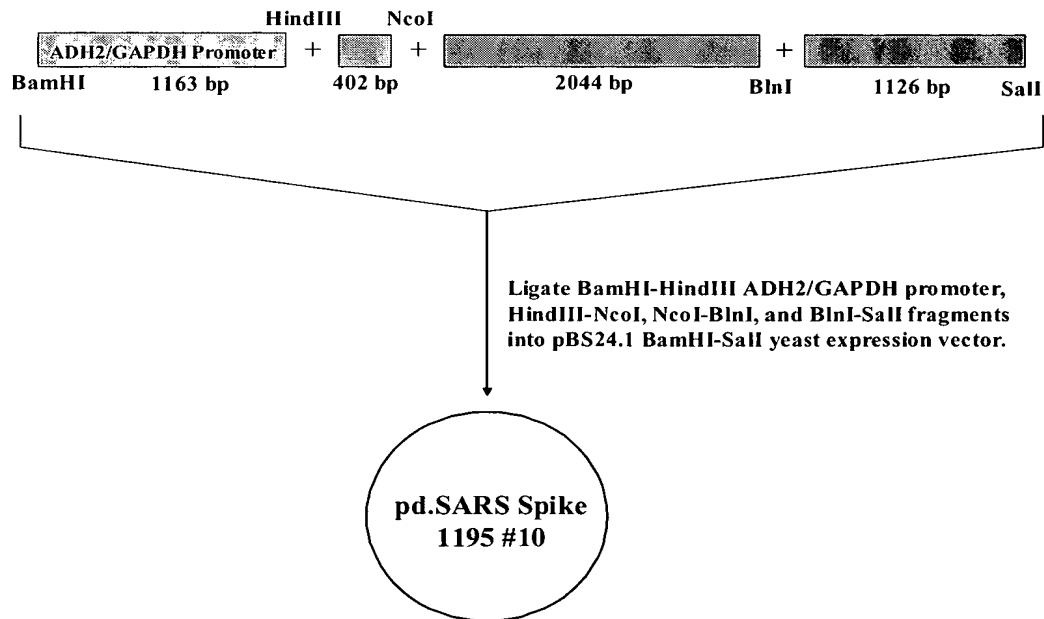
**FIGURE 57****FIGURE 58**

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**FIGURE 59****FIGURE 60**

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**FIGURE 61****FIGURE 62**

**FIGURE 63****FIGURE 64**

**FIGURE 65**

					1										10
AAGCTTACAAAACAAA					M	S	D	L	D	R	C	T	T	F	
					ATG	AGT	GAC	CTT	GAC	CGG	TGC	ACC	ACT	TTT	
					20										
D	D	V	Q	A	P	N	Y	T	Q	H	T	S	S	M	
GAT	GAT	GTT	CAA	GCT	CCT	AAT	TAC	ACT	CAA	CAT	ACT	TCA	TCT	ATG	
					30										40
R	G	V	Y	Y	P	D	E	I	F	R	S	D	T	L	
AGG	GGG	GTT	TAC	TAT	CCT	GAT	GAA	ATT	TTT	AGA	TCA	GAC	ACT	CTT	
					50										
Y	L	T	Q	D	L	F	L	P	F	Y	S	N	V	T	
TAT	TTA	ACT	CAG	GAT	TTA	TTT	CTT	CCA	TTT	TAT	TCT	AAT	GTT	ACA	
					60										70
G	F	H	T	I	N	H	T	F	G	N	P	V	I	P	
GGG	TTT	CAT	ACT	ATT	AAT	CAT	ACG	TTT	GGC	AAC	CCT	GTC	ATA	CCT	
					80										
F	K	D	G	I	Y	F	A	A	T	E	K	S	N	V	
TTT	AAG	GAT	GGT	ATT	TAT	TTT	GCT	GCC	ACA	GAG	AAA	TCA	AAT	GTT	
					90										100
V	R	G	W	V	F	G	S	T	M	N	N	K	S	Q	
GTC	CGT	GGT	TGG	GTT	TTT	GGT	TCT	ACC	ATG	AAC	AAC	AAG	TCA	CAG	
					110										
S	V	I	I	I	N	N	S	T	N	V	V	I	R	A	
TCG	GTG	ATT	ATT	ATT	AAC	AAT	TCT	ACT	AAT	GTT	GTT	ATA	CGA	GCA	
					120										130
C	N	F	E	L	C	D	N	P	F	F	A	V	S	K	
TGT	AAC	TTT	GAA	TTG	TGT	GAC	AAC	CCT	TTC	TTT	GCT	GTT	TCT	AAA	
					140										
P	M	G	T	Q	T	H	T	M	I	F	D	N	A	F	
CCC	ATG	GGT	ACA	CAG	ACA	CAT	ACT	ATG	ATA	TTC	GAT	AAT	GCA	TTT	
					150										160
N	C	T	F	E	Y	I	S	D	A	F	S	L	D	V	
AAT	TGC	ACT	TTC	GAG	TAC	ATA	TCT	GAT	GCC	TTT	TCG	CTT	GAT	GTT	
					170										
S	E	K	S	G	N	F	K	H	L	R	E	F	V	F	
TCA	GAA	AAG	TCA	GGT	AAT	TTT	AAA	CAC	TTA	CGA	GAG	TTT	GTG	TTT	
					180										190
K	N	K	D	G	F	L	Y	V	Y	K	G	Y	Q	P	
AAA	AAT	AAA	GAT	GGG	TTT	CTC	TAT	GTT	TAT	AAG	GGC	TAT	CAA	CCT	

```

                200
  I   D   V   V   R   D   L   P   S   G   F   N   T   L   K
ATA GAT GTA GTT CGT GAT CTA CCT TCT GGT TTT AAC ACT TTG AAA

                210
  P   I   F   K   L   P   L   G   I   N   I   T   N   F   R
CCT ATT TTT AAG TTG CCT CTT GGT ATT AAC ATT ACA AAT TTT AGA

                230
  A   I   L   T   A   F   S   P   A   Q   D   I   W   G   T
GCC ATT CTT ACA GCC TTT TCA CCT GCT CAA GAC ATT TGG GGC ACG

                240
  S   A   A   A   Y   F   V   G   Y   L   K   P   T   T   F
TCA GCT GCA GCC TAT TTT GTT GGC TAT TTA AAG CCA ACT ACA TTT

                260
  M   L   K   Y   D   E   N   G   T   I   T   D   A   V   D
ATG CTC AAG TAT GAT GAA AAT GGT ACA ATC ACA GAT GCT GTT GAT

                270
  C   S   Q   N   P   L   A   E   L   K   C   S   V   K   S
TGT TCT CAA AAT CCA CTT GCT GAA CTC AAA TGC TCT GTT AAG AGC

                290
  F   E   I   D   K   G   I   Y   Q   T   S   N   F   R   V
TTT GAG ATT GAC AAA GGA ATT TAC CAG ACC TCT AAT TTC AGG GTT

                300
  V   P   S   G   D   V   V   R   F   P   N   I   T   N   L
GTT CCC TCA GGA GAT GTT GTG AGA TTC CCT AAT ATT ACA AAC TTG

                320
  C   P   F   G   E   V   F   N   A   T   K   F   P   S   V
TGT CCT TTT GGA GAG GTT TTT AAT GCT ACT AAA TTC CCT TCT GTC

                330
  Y   A   W   E   R   K   K   I   S   N   C   V   A   D   Y
TAT GCA TGG GAG AGA AAA AAA ATT TCT AAT TGT GTT GCT GAT TAC

                350
  S   V   L   Y   N   S   T   F   F   S   T   F   K   C   Y
TCT GTG CTC TAC AAC TCA ACA TTT TTT TCA ACC TTT AAG TGC TAT

                360
  G   V   S   A   T   K   L   N   D   L   C   F   S   N   V
GGC GTT TCT GCC ACT AAG TTG AAT GAT CTT TGC TTC TCC AAT GTC

                380
  Y   A   D   S   F   V   V   K   G   D   D   V   R   Q   I
TAT GCA GAT TCT TTT GTA GTC AAG GGA GAT GAT GTA AGA CAA ATA

                390
  A   P   G   Q   T   G   V   I   A   D   Y   N   Y   K   L
GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG

```



```

                                410
    P   D   D   F   M   G   C   V   L   A   W   N   T   R   N
CCA GAT GAT TTC ATG GGT TGT GTC CTT GCT TGG AAT ACT AGG AAC

                                420
    I   D   A   T   S   T   G   N   Y   N   Y   K   Y   R   Y
ATT GAT GCT ACT TCA ACT GGT AAT TAT AAT TAT AAA TAT AGG TAT

                                440
    L   R   H   G   K   L   R   P   F   E   R   D   I   S   N
CTT AGA CAT GGC AAG CTT AGG CCC TTT GAG AGA GAC ATA TCT AAT

                                450
    V   P   F   S   P   D   G   K   P   C   T   P   P   A   L
GTG CCT TTC TCC CCT GAT GGC AAA CCT TGC ACC CCA CCT GCT CTT

                                470
    N   C   Y   W   P   L   N   D   Y   G   F   Y   T   T   T
AAT TGT TAT TGG CCA TTA AAT GAT TAT GGT TTT TAC ACC ACT ACT

                                480
    G   I   G   Y   Q   P   Y   R   V   V   V   L   S   F   E
GGC ATT GGC TAC CAA CCT TAC AGA GTT GTA GTA CTT TCT TTT GAA

                                500
    L   L   N   A   P   A   T   V   C   G   P   K   L   S   T
CTT TTA AAT GCA CCG GCC ACG GTT TGT GGA CCA AAA TTA TCC ACT

                                510
    D   L   I   K   N   Q   C   V   N   F   N   F   N   G   L
GAC CTT ATT AAG AAC CAG TGT GTC AAT TTT AAT TTT AAT GGA CTC

                                530
    T   G   T   G   V   L   T   P   S   S   K   R   F   Q   P
ACT GGT ACT GGT GTG TTA ACT CCT TCT TCA AAG AGA TTT CAA CCA

                                540
    F   Q   Q   F   G   R   D   V   S   D   F   T   D   S   V
TTT CAA CAA TTT GGC CGT GAT GTT TCT GAT TTC ACT GAT TCC GTT

                                560
    R   D   P   K   T   S   E   I   L   D   I   S   P   C   S
CGA GAT CCT AAA ACA TCT GAA ATA TTA GAC ATT TCA CCT TGC TCT

                                570
    F   G   G   V   S   V   I   T   P   G   T   N   A   S   S
TTT GGG GGT GTA AGT GTA ATT ACA CCT GGA ACA AAT GCT TCA TCT

                                590
    E   V   A   V   L   Y   Q   D   V   N   C   T   D   V   S
GAA GTT GCT GTT CTA TAT CAA GAT GTT AAC TGC ACT GAT GTT TCT

                                600
    T   A   I   H   A   D   Q   L   T   P   A   W   R   I   Y

```

ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT

620

S T G N N V F Q T Q A G C L I  
TCT ACT GGA AAC AAT GTA TTC CAG ACT CAA GCA GGC TGT CTT ATA

630

640

G A E H V D T S Y E C D I P I  
GGA GCT GAG CAT GTT GAT ACT TCT TAT GAG TGC GAC ATT CCT ATT

650

G A G I C A S Y H T OC  
GGA GCT GGC ATT TGT GCT AGT TAC CAT ACA TAA TGAGTCGAC

SEQ ID NO: 9799

SEQ ID NO: 9800

Translated Mol. Weight = 72525.52

**FIGURE 66**

1 10  
M S D L D R C T T F  
AAGCTTACAAAACAAA ATG AGT GAC CTT GAC CGG TGC ACC ACT TTT

20  
D D V Q A P N Y T Q H T S S M  
GAT GAT GTT CAA GCT CCT AAT TAC ACT CAA CAT ACT TCA TCT ATG

30 40  
R G V Y Y P D E I F R S D T L  
AGG GGG GTT TAC TAT CCT GAT GAA ATT TTT AGA TCA GAC ACT CTT

50  
Y L T Q D L F L P F Y S N V T  
TAT TTA ACT CAG GAT TTA TTT CTT CCA TTT TAT TCT AAT GTT ACA

60 70  
G F H T I N H T F G N P V I P  
GGG TTT CAT ACT ATT AAT CAT ACG TTT GGC AAC CCT GTC ATA CCT

80  
F K D G I Y F A A T E K S N V  
TTT AAG GAT GGT ATT TAT TTT GCT GCC ACA GAG AAA TCA AAT GTT

90 100  
V R G W V F G S T M N N K S Q  
GTC CGT GGT TGG GTT TTT GGT TCT ACC ATG AAC AAC AAG TCA CAG

110  
S V I I I N N S T N V V I R A  
TCG GTG ATT ATT ATT AAC AAT TCT ACT AAT GTT GTT ATA CGA GCA

120 130  
C N F E L C D N P F F A V S K  
TGT AAC TTT GAA TTG TGT GAC AAC CCT TTC TTT GCT GTT TCT AAA

140  
P M G T Q T H T M I F D N A F  
CCC ATG GGT ACA CAG ACA CAT ACT ATG ATA TTC GAT AAT GCA TTT

150 160  
N C T F E Y I S D A F S L D V

```

AAT TGC ACT TTC GAG TAC ATA TCT GAT GCC TTT TCG CTT GAT GTT
                                170
  S   E   K   S   G   N   F   K   H   L   R   E   F   V   F
TCA GAA AAG TCA GGT AAT TTT AAA CAC TTA CGA GAG TTT GTG TTT

                                180                                190
  K   N   K   D   G   F   L   Y   V   Y   K   G   Y   Q   P
AAA AAT AAA GAT GGG TTT CTC TAT GTT TAT AAG GGC TAT CAA CCT

                                200
  I   D   V   V   R   D   L   P   S   G   F   N   T   L   K
ATA GAT GTA GTT CGT GAT CTA CCT TCT GGT TTT AAC ACT TTG AAA

                                210                                220
  P   I   F   K   L   P   L   G   I   N   I   T   N   F   R
CCT ATT TTT AAG TTG CCT CTT GGT ATT AAC ATT ACA AAT TTT AGA

                                230
  A   I   L   T   A   F   S   P   A   Q   D   I   W   G   T
GCC ATT CTT ACA GCC TTT TCA CCT GCT CAA GAC ATT TGG GGC ACG

                                240                                250
  S   A   A   A   Y   F   V   G   Y   L   K   P   T   T   F
TCA GCT GCA GCC TAT TTT GTT GGC TAT TTA AAG CCA ACT ACA TTT

                                260
  M   L   K   Y   D   E   N   G   T   I   T   D   A   V   D
ATG CTC AAG TAT GAT GAA AAT GGT ACA ATC ACA GAT GCT GTT GAT

                                270                                280
  C   S   Q   N   P   L   A   E   L   K   C   S   V   K   S
TGT TCT CAA AAT CCA CTT GCT GAA CTC AAA TGC TCT GTT AAG AGC

                                290
  F   E   I   D   K   G   I   Y   Q   T   S   N   F   R   V
TTT GAG ATT GAC AAA GGA ATT TAC CAG ACC TCT AAT TTC AGG GTT

                                300                                310
  V   P   S   G   D   V   V   R   F   P   N   I   T   N   L
GTT CCC TCA GGA GAT GTT GTG AGA TTC CCT AAT ATT ACA AAC TTG

                                320
  C   P   F   G   E   V   F   N   A   T   K   F   P   S   V
TGT CCT TTT GGA GAG GTT TTT AAT GCT ACT AAA TTC CCT TCT GTC

                                330                                340
  Y   A   W   E   R   K   K   I   S   N   C   V   A   D   Y
TAT GCA TGG GAG AGA AAA AAA ATT TCT AAT TGT GTT GCT GAT TAC

                                350
  S   V   L   Y   N   S   T   F   F   S   T   F   K   C   Y
TCT GTG CTC TAC AAC TCA ACA TTT TTT TCA ACC TTT AAG TGC TAT

                                360                                370
  G   V   S   A   T   K   L   N   D   L   C   F   S   N   V
GGC GTT TCT GCC ACT AAG TTG AAT GAT CTT TGC TTC TCC AAT GTC

                                380
  Y   A   D   S   F   V   V   K   G   D   D   V   R   Q   I
TAT GCA GAT TCT TTT GTA GTC AAG GGA GAT GAT GTA AGA CAA ATA

                                390                                400

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A P G Q T G V I A D Y N Y K L  
 GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG  
 410  
 P D D F M G C V L A W N T R N  
 CCA GAT GAT TTC ATG GGT TGT GTC CTT GCT TGG AAT ACT AGG AAC  
 420 430  
 I D A T S T G N Y N Y K Y R Y  
 ATT GAT GCT ACT TCA ACT GGT AAT TAT AAT TAT AAA TAT AGG TAT  
 440  
 L R H G K L R P F E R D I S N  
 CTT AGA CAT GGC AAG CTT AGG CCC TTT GAG AGA GAC ATA TCT AAT  
 450 460  
 V P F S P D G K P C T P P A L  
 GTG CCT TTC TCC CCT GAT GGC AAA CCT TGC ACC CCA CCT GCT CTT  
 470  
 N C Y W P L N D Y G F Y T T T  
 AAT TGT TAT TGG CCA TTA AAT GAT TAT GGT TTT TAC ACC ACT ACT  
 480 490  
 G I G Y Q P Y R V V V L S F E  
 GGC ATT GGC TAC CAA CCT TAC AGA GTT GTA GTA CTT TCT TTT GAA  
 500  
 L L N A P A T V C G P K L S T  
 CTT TTA AAT GCA CCG GCC ACG GTT TGT GGA CCA AAA TTA TCC ACT  
 510 520  
 D L I K N Q C V N F N F N G L  
 GAC CTT ATT AAG AAC CAG TGT GTC AAT TTT AAT TTT AAT GGA CTC  
 530  
 T G T G V L T P S S K R F Q P  
 ACT GGT ACT GGT GTG TTA ACT CCT TCT TCA AAG AGA TTT CAA CCA  
 540 550  
 F Q Q F G R D V S D F T D S V  
 TTT CAA CAA TTT GGC CGT GAT GTT TCT GAT TTC ACT GAT TCC GTT  
 560  
 R D P K T S E I L D I S P C S  
 CGA GAT CCT AAA ACA TCT GAA ATA TTA GAC ATT TCA CCT TGC TCT  
 570 580  
 F G G V S V I T P G T N A S S  
 TTT GGG GGT GTA AGT GTA ATT ACA CCT GGA ACA AAT GCT TCA TCT  
 590  
 E V A V L Y Q D V N C T D V S  
 GAA GTT GCT GTT CTA TAT CAA GAT GTT AAC TGC ACT GAT GTT TCT  
 600 610  
 T A I H A D Q L T P A W R I Y  
 ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT  
 620  
 S T G N N V F Q T Q A G C L I  
 TCT ACT GGA AAC AAT GTA TTC CAG ACT CAA GCA GGC TGT CTT ATA

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      630
G   A   E   H   V   D   T   S   Y   E   C   D   I   P   I
GGA GCT GAG CAT GTC GAC ACT TCT TAT GAG TGC GAC ATT CCT ATT

      650
G   A   G   I   C   A   S   Y   H   T   V   S   L   L   R
GGA GCT GGC ATT TGT GCT AGT TAC CAT ACA GTT TCT TTA TTA CGT

      660
S   T   S   Q   K   S   I   V   A   Y   T   M   S   L   G
AGT ACT AGC CAA AAA TCT ATT GTG GCT TAT ACT ATG TCT TTA GGT

      680
A   D   S   S   I   A   Y   S   N   N   T   I   A   I   P
GCT GAT AGT TCA ATT GCT TAC TCT AAT AAC ACC ATT GCT ATA CCT

      690
T   N   F   S   I   S   I   T   T   E   V   M   P   V   S
ACT AAC TTT TCA ATT AGC ATT ACT ACA GAA GTA ATG CCT GTT TCT

      710
M   A   K   T   S   V   D   C   N   M   Y   I   C   G   D
ATG GCT AAA ACC TCC GTA GAT TGT AAT ATG TAC ATC TGC GGA GAT

      720
S   T   E   C   A   N   L   L   L   Q   Y   G   S   F   C
TCT ACT GAA TGT GCT AAT TTG CTT CTC CAA TAT GGT AGC TTT TGC

      740
T   Q   L   N   R   A   L   S   G   I   A   A   E   Q   D
ACA CAA CTA AAT CGT GCA CTC TCA GGT ATT GCT GCT GAA CAG GAT

      750
R   N   T   R   E   V   F   A   Q   V   K   Q   M   Y   K
CGC AAC ACA CGT GAA GTG TTC GCT CAA GTC AAA CAA ATG TAC AAA

      770
T   P   T   L   K   Y   F   G   G   F   N   F   S   Q   I
ACC CCA ACT TTG AAA TAT TTT GGT GGT TTT AAT TTT TCA CAA ATA

      780
L   P   D   P   L   K   P   T   K   R   S   F   I   E   D
TTA CCT GAC CCT CTA AAG CCA ACT AAG AGG TCT TTT ATT GAG GAC

      800
L   L   F   N   K   V   T   L   A   D   A   G   F   M   K
TTG CTC TTT AAT AAG GTG ACA CTC GCT GAT GCT GGC TTC ATG AAG

      810
Q   Y   G   E   C   L   G   D   I   N   A   R   D   L   I
CAA TAT GGC GAA TGC CTA GGT GAT ATT AAT GCT AGG GAC CTC ATT

      830
C   A   Q   K   F   N   G   L   T   V   L   P   P   L   L
TGT GCG CAG AAG TTC AAT GGA CTT ACA GTG TTG CCA CCT CTG CTC

      840
T   D   D   M   I   A   A   Y   T   A   A   L   V   S   G
ACT GAT GAT ATG ATT GCT GCC TAC ACT GCT GCT CTA GTT AGT GGT

      860
T   A   T   A   G   W   T   F   G   A   G   A   A   L   Q
ACT GCC ACT GCT GGA TGG ACA TTT GGT GCT GGC GCT GCT CTT CAA

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      870                                     880
    I   P   F   A   M   Q   M   A   Y   R   F   N   G   I   G
    ATA CCT TTT GCT ATG CAA ATG GCA TAT AGG TTC AAT GGC ATT GGA

                                     890
    V   T   Q   N   V   L   Y   E   N   Q   K   Q   I   A   N
    GTT ACC CAA AAT GTT CTC TAT GAG AAC CAA AAA CAA ATC GCC AAC

      900                                     910
    Q   F   N   K   A   I   S   Q   I   Q   E   S   L   T   T
    CAA TTT AAC AAG GCG ATT AGT CAA ATT CAA GAA TCA CTT ACA ACA

                                     920
    T   S   T   A   L   G   K   L   Q   D   V   V   N   Q   N
    ACA TCA ACT GCA TTG GGC AAG CTG CAA GAC GTT GTT AAC CAG AAT

      930                                     940
    A   Q   A   L   N   T   L   V   K   Q   L   S   S   N   F
    GCT CAA GCA TTA AAC ACA CTT GTT AAA CAA CTT AGC TCT AAT TTT

                                     950
    G   A   I   S   S   V   L   N   D   I   L   S   R   L   D
    GGT GCA ATT TCA AGT GTG CTA AAT GAT ATC CTT TCG CGA CTT GAT

      960                                     970
    K   V   E   A   E   V   Q   I   D   R   L   I   T   G   R
    AAA GTC GAG GCG GAG GTA CAA ATT GAC AGG TTA ATT ACA GGC AGA

                                     980
    L   Q   S   L   Q   T   Y   V   T   Q   Q   L   I   R   A
    CTT CAA AGC CTT CAA ACC TAT GTA ACA CAA CAA CTA ATC AGG GCT

      990                                     1000
    A   E   I   R   A   S   A   N   L   A   A   T   K   M   S
    GCT GAA ATC AGG GCT TCT GCT AAT CTT GCT GCT ACT AAA ATG TCT

                                     1010
    E   C   V   L   G   Q   S   K   R   V   D   F   C   G   K
    GAG TGT GTT CTT GGA CAA TCA AAA AGA GTT GAC TTT TGT GGA AAG

      1020                                     1030
    G   Y   H   L   M   S   F   P   Q   A   A   P   H   G   V
    GGC TAC CAC CTT ATG TCC TTC CCA CAA GCA GCC CCG CAT GGT GTT

                                     1040
    V   F   L   H   V   T   Y   V   P   S   Q   E   R   N   F
    GTC TTC CTA CAT GTC ACG TAT GTG CCA TCC CAG GAG AGG AAC TTC

      1050                                     1060
    T   T   A   P   A   I   C   H   E   G   K   A   Y   F   P
    ACC ACA GCG CCA GCA ATT TGT CAT GAA GGC AAA GCA TAC TTC CCT

                                     1070
    R   E   G   V   F   V   F   N   G   T   S   W   F   I   T
    CGT GAA GGT GTT TTT GTG TTT AAT GGC ACT TCT TGG TTT ATT ACA

      1080                                     1090
    Q   R   N   F   F   S   P   Q   I   I   T   T   D   N   T
    CAG AGG AAC TTC TTT TCT CCA CAA ATA ATT ACT ACA GAC AAT ACA

                                     1100
    F   V   S   G   N   C   D   V   V   I   G   I   I   N   N

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TTT GTC TCA GGA AAT TGT GAT GTC GTT ATT GGC ATC ATT AAC AAC  
1110 1120  
T V Y D P L Q P E L D S F K E  
ACA GTT TAT GAT CCT CTG CAA CCT GAG CTT GAC TCA TTC AAA GAA  
1130  
E L D K Y F K N H T S P D V D  
GAG CTG GAC AAG TAC TTC AAA AAT CAT ACA TCA CCA GAT GTT GAT  
1140 1150  
F G D I S G I N A S V V N I Q  
TTT GGC GAC ATT TCA GGC ATT AAC GCT TCT GTC GTC AAC ATT CAA  
1160  
K E I D R L N E V A K N L N E  
AAA GAA ATT GAC CGC CTC AAT GAG GTC GCT AAA AAT TTA AAT GAA  
1170 1180  
S L I D L Q E L G K Y E Q Y I  
TCA CTC ATT GAC CTT CAA GAA TTG GGA AAA TAT GAG CAA TAT ATT  
1183  
K W P OC  
AAA TGG CCT TAA TGAGTCGAC  
SEQ ID NO: 9801  
SEQ ID NO: 9802

Translated Mol. Weight = 131315.20

FIGURE 67

FIGURE 67A

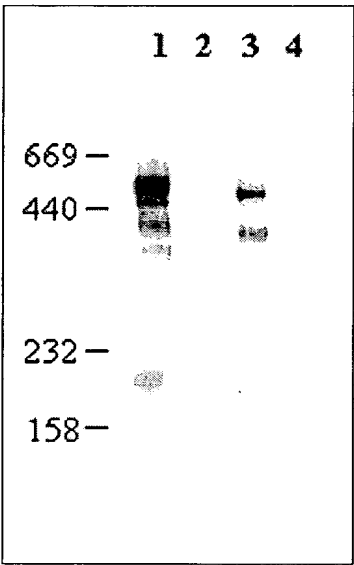
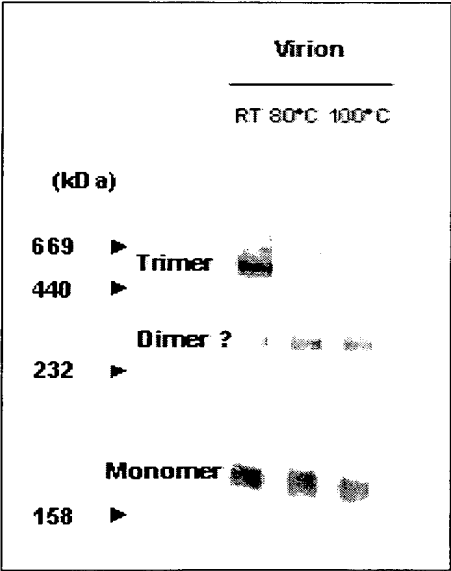
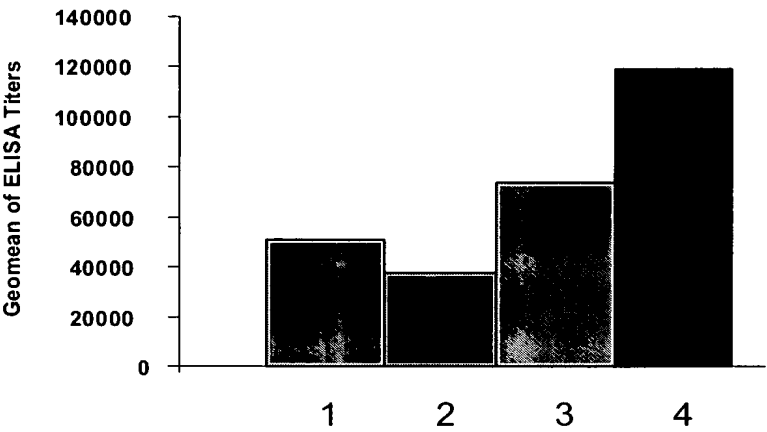


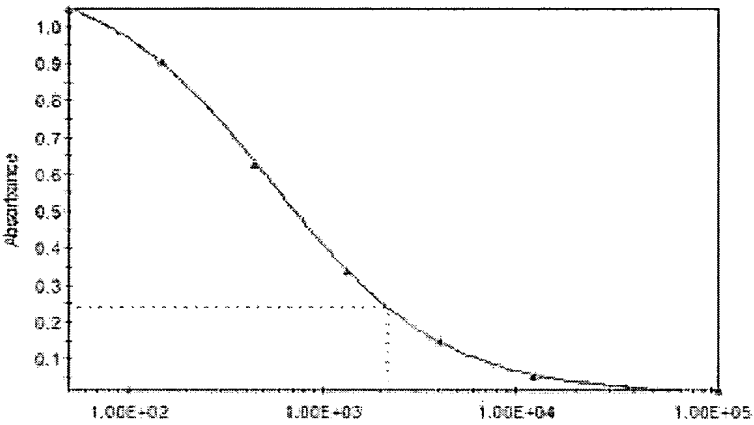
FIGURE 67B



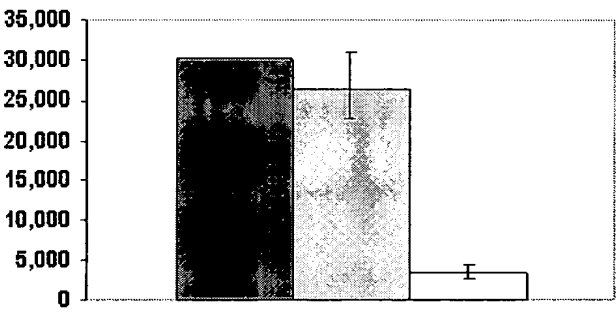
**FIGURE 68**



**FIGURE 69**



**FIGURE 70**





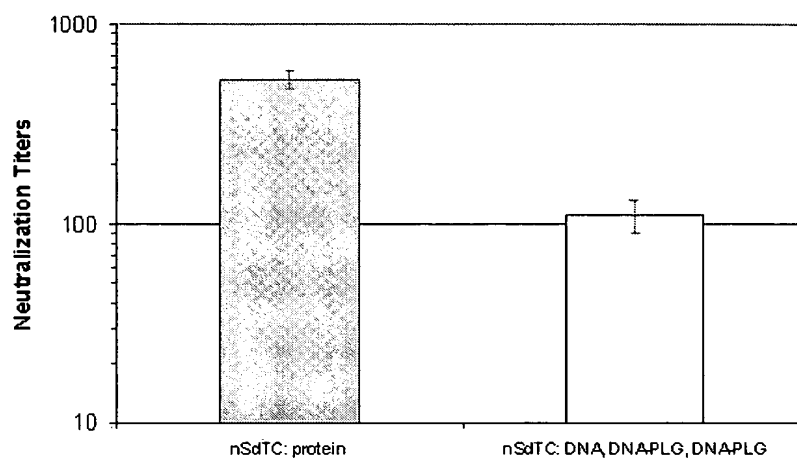
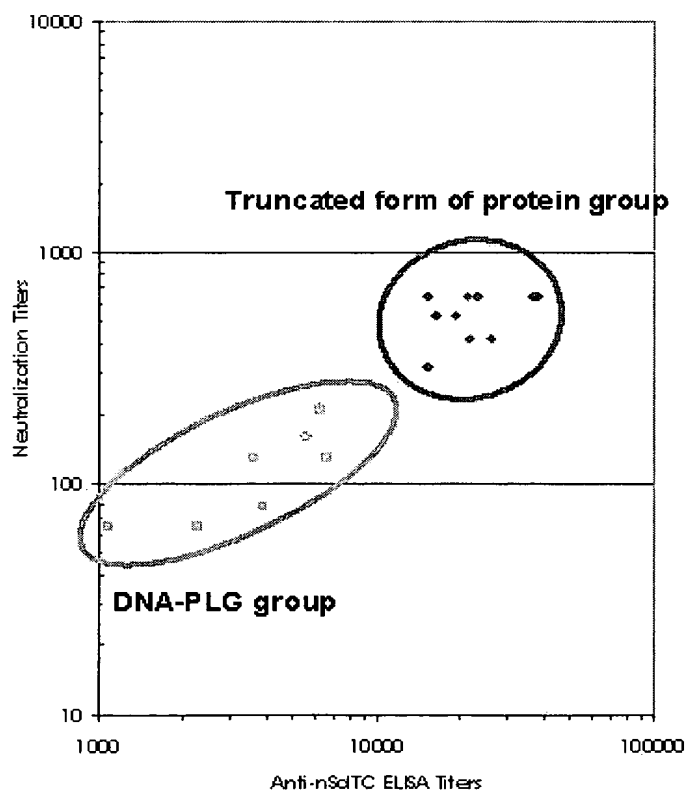
**FIGURE 71****FIGURE 72**

FIGURE 73

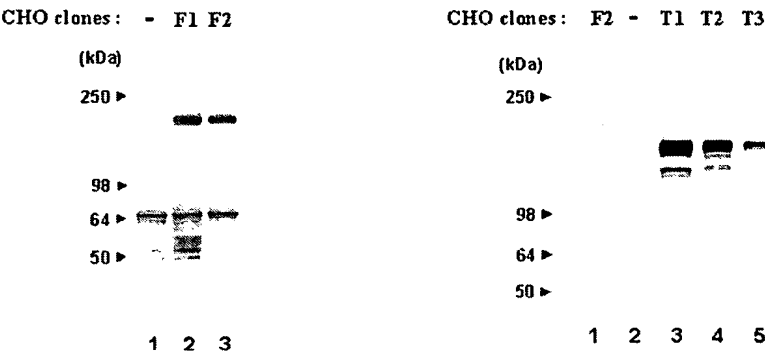


FIGURE 74

FIGURE 74A

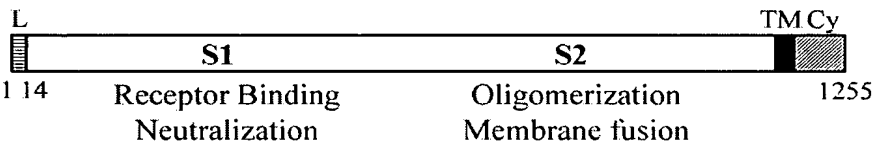


FIGURE 74B

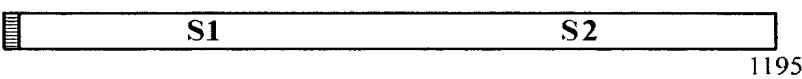


FIGURE 75

FIGURE 75A

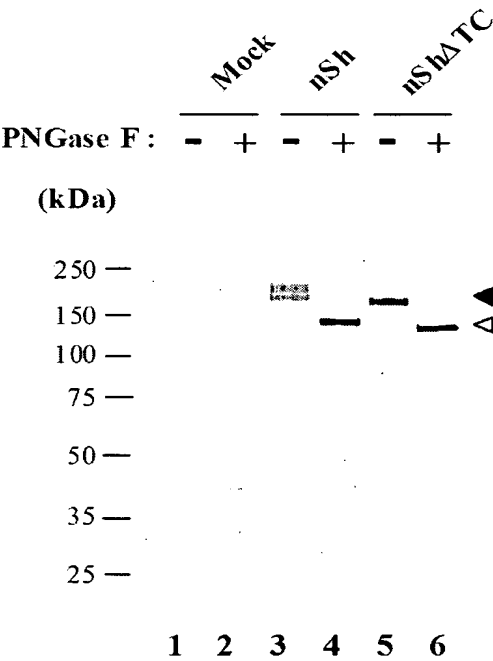
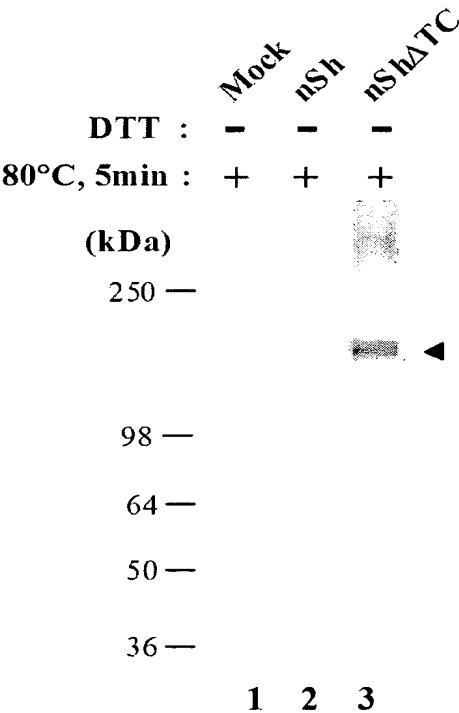
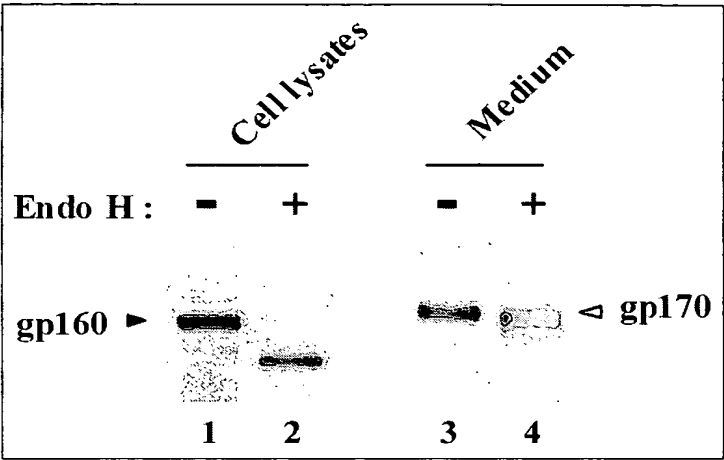


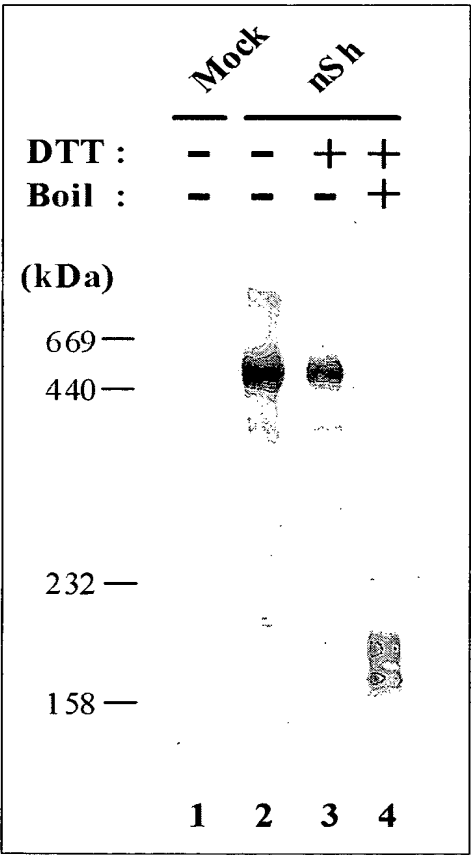
FIGURE 75B



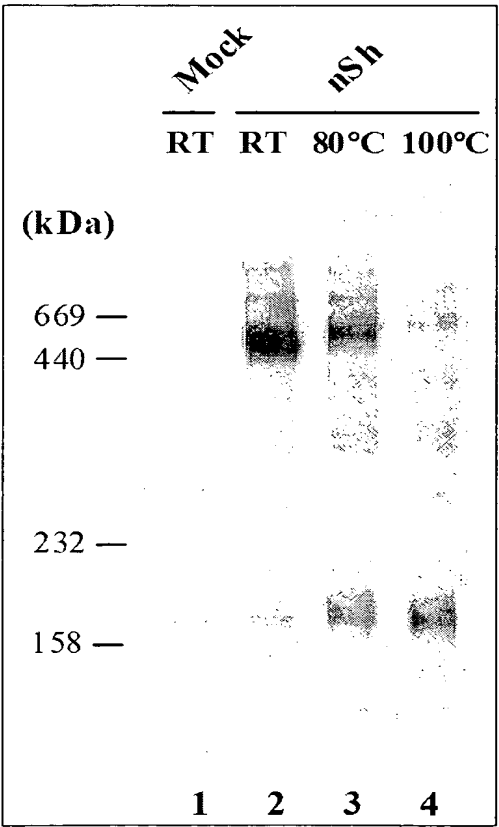
**FIGURE 76**



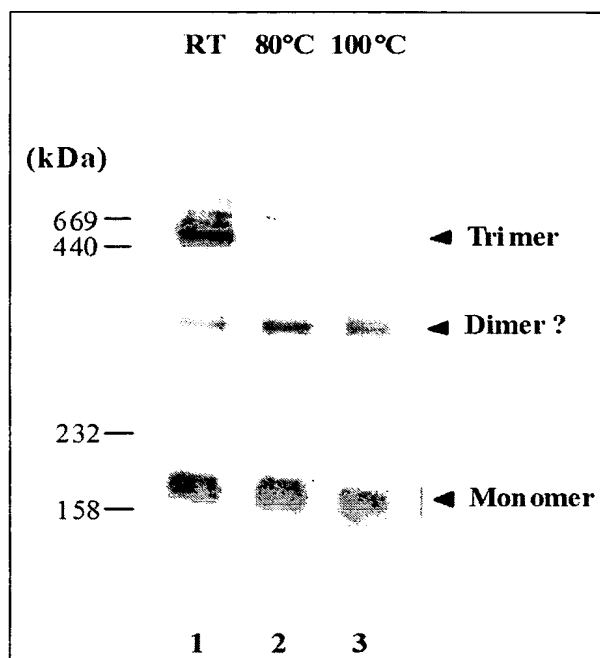
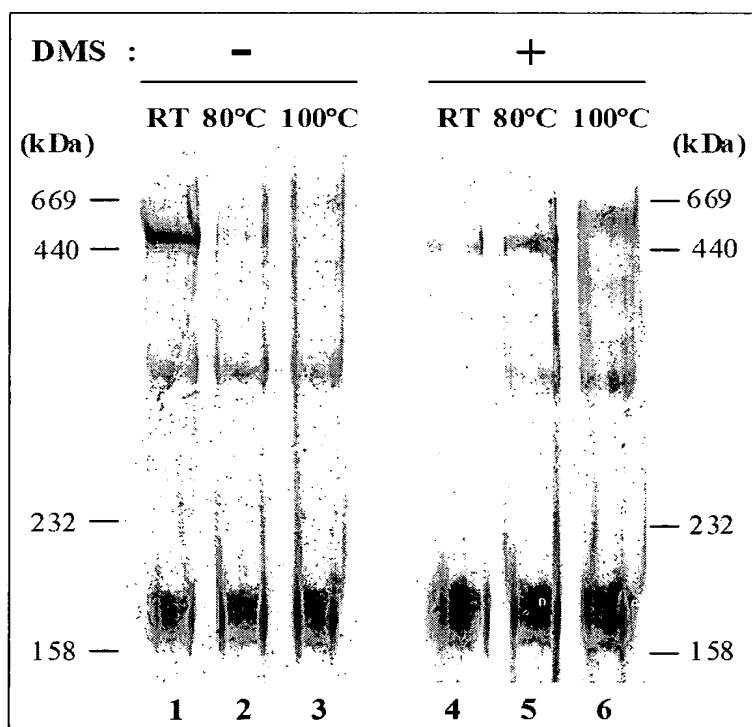
**FIGURE 77**



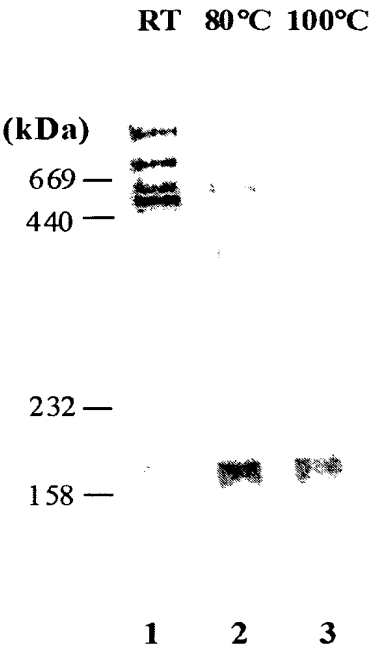
**FIGURE 78**



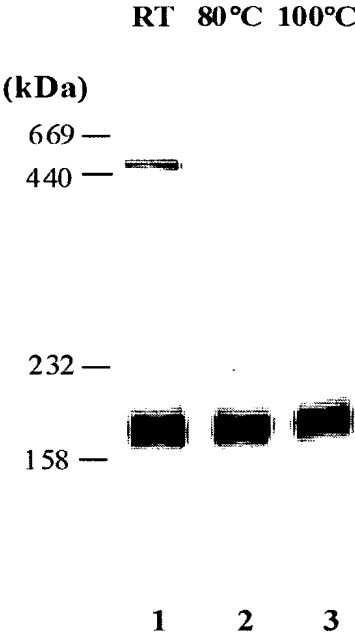
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**FIGURE 79****FIGURE 80**

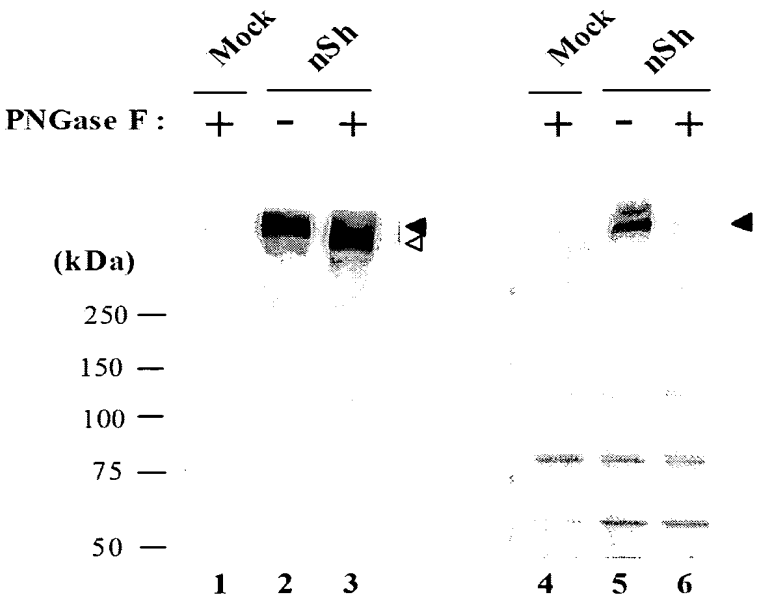
**FIGURE 81**



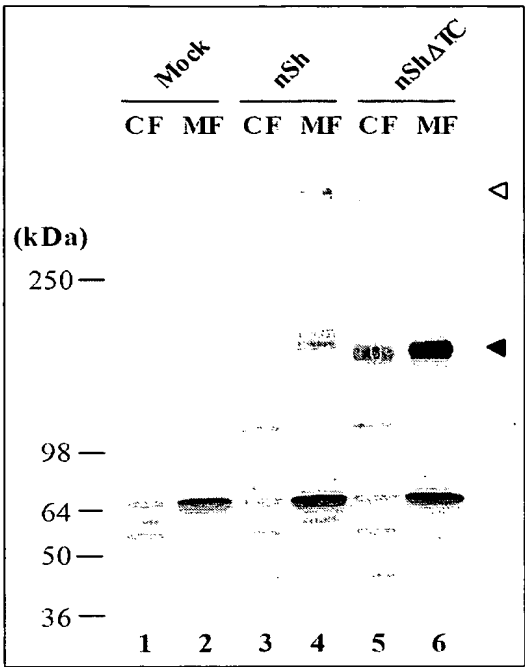
**FIGURE 82**



**FIGURE 83**

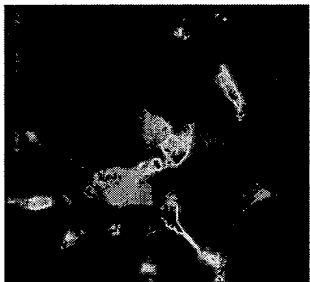


**FIGURE 84**

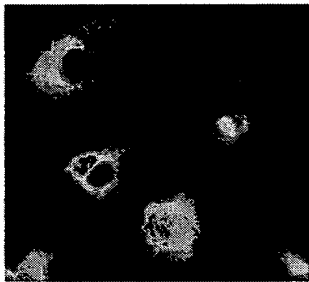


**FIGURE 85**

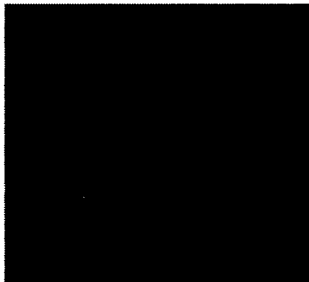
**FIGURE 85A**



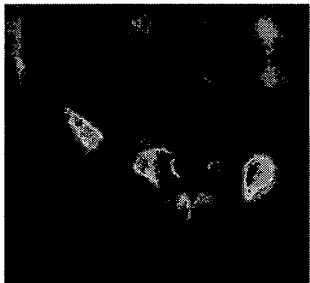
**FIGURE 85B**



**FIGURE 85C**



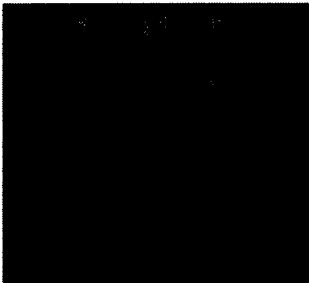
**FIGURE 85D**



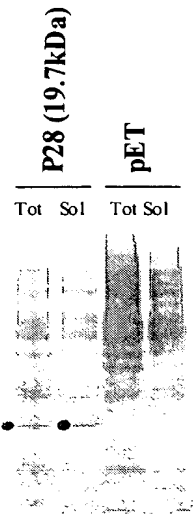
**FIGURE 85E**



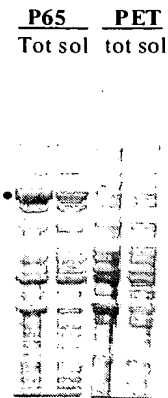
**FIGURE 85F**



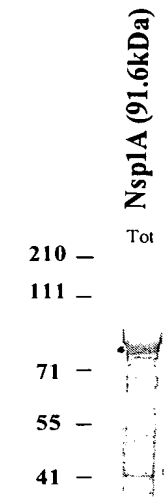
**FIGURE 86**



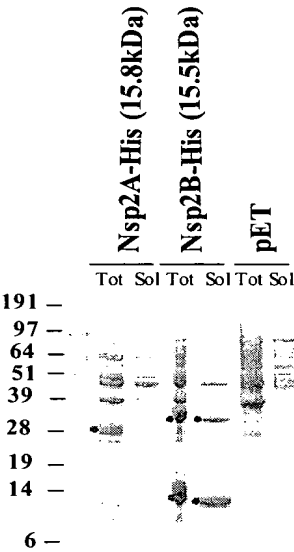
**FIGURE 87**



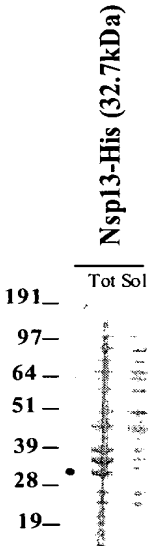
**FIGURE 88**



**FIGURE 89**



**FIGURE 90**



**FIGURE 91**

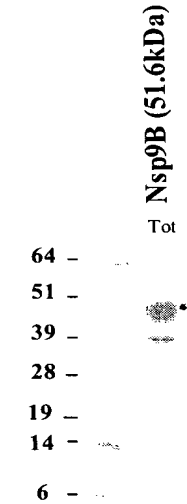


FIGURE 92

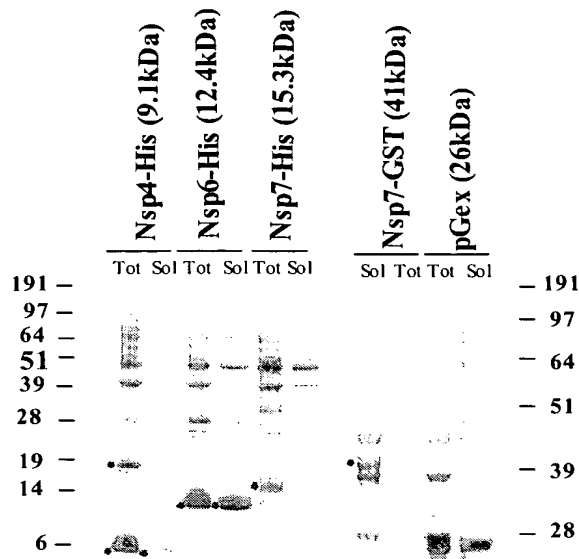


FIGURE 93

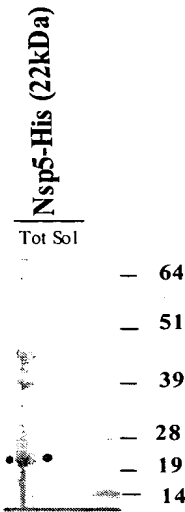


FIGURE 94

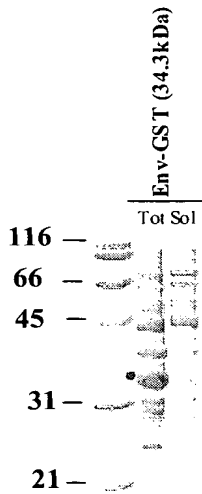


FIGURE 95

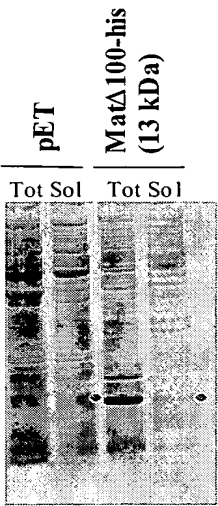
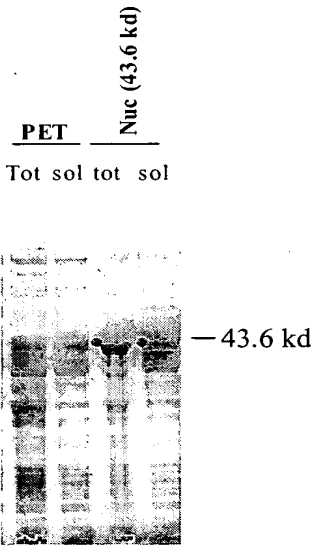
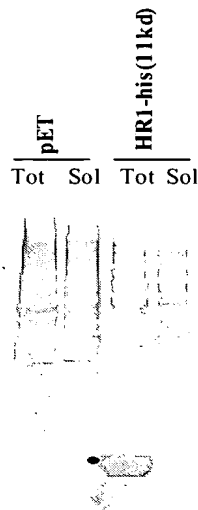


FIGURE 96

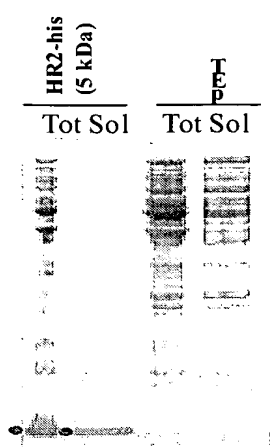




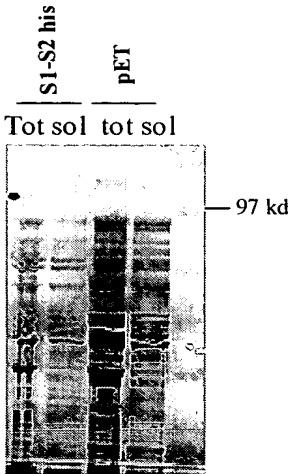
**FIGURE 97**



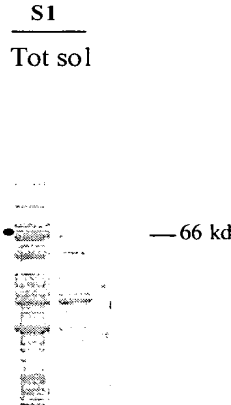
**FIGURE 98**



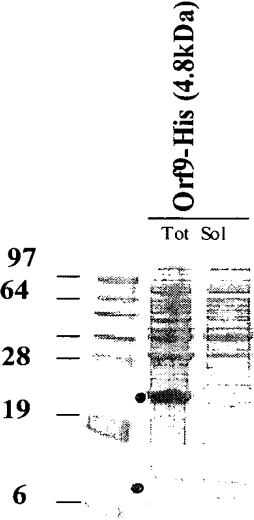
**FIGURE 99**



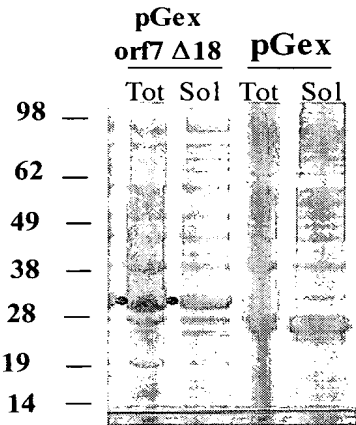
**FIGURE 100**



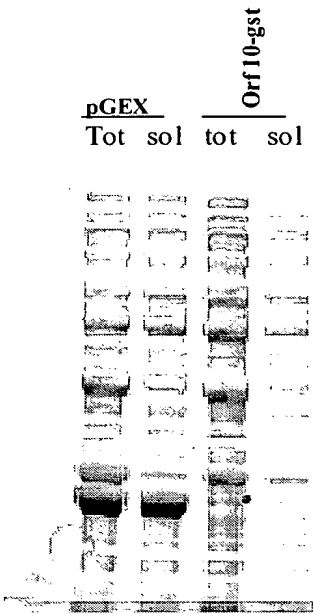
**FIGURE 101**



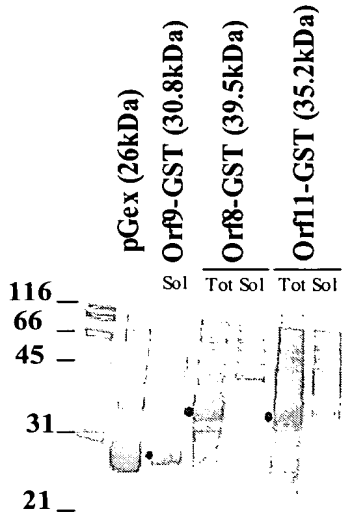
**FIGURE 102**



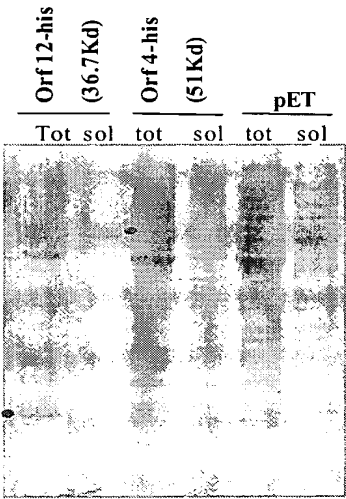
**FIGURE 103**



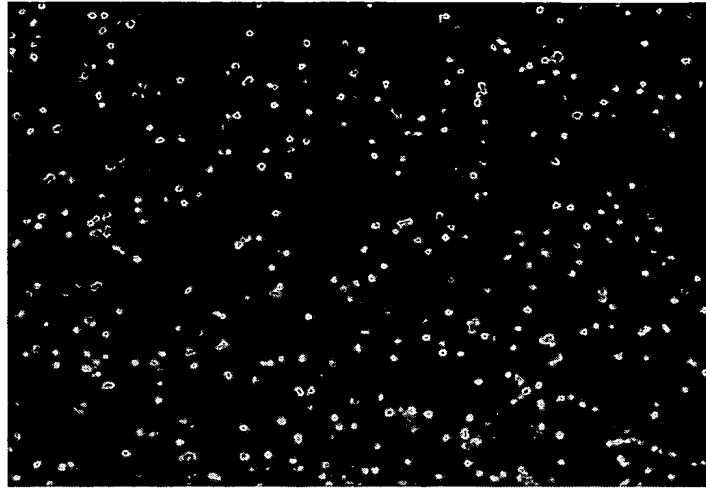
**FIGURE 104**



**FIGURE 105**

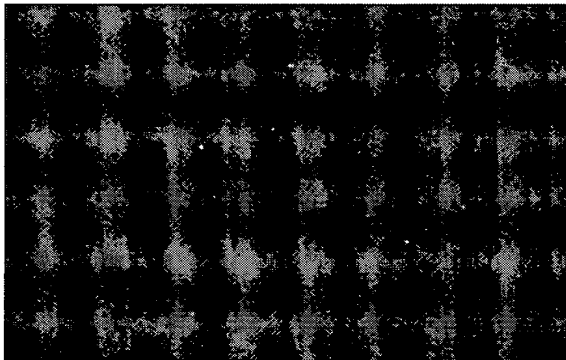


**FIGURE 106**

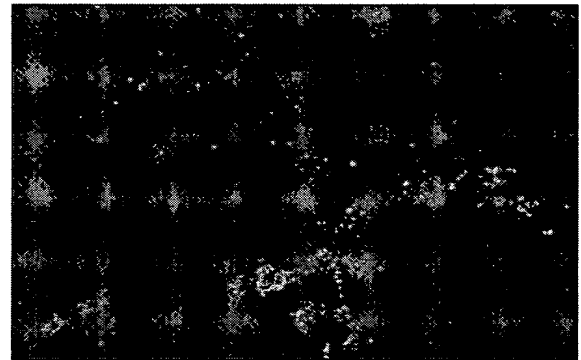


**FIGURE 107**

**FIGURE 107A**



**FIGURE 107B**



**FIGURE 108**

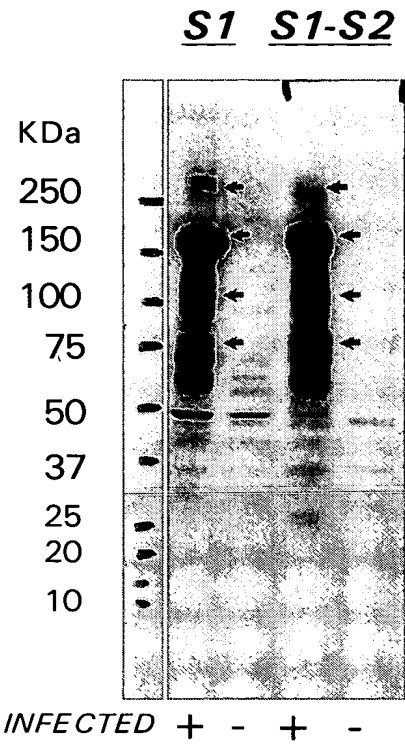
**FIGURE 108A**



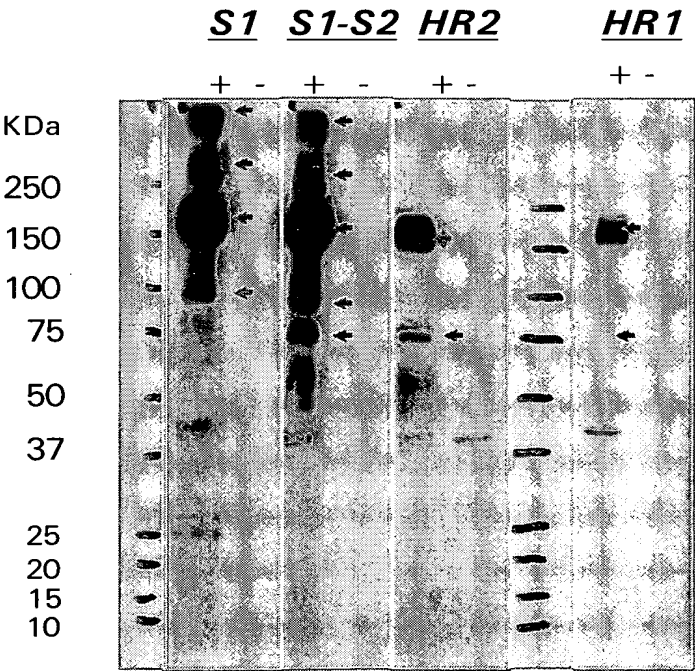
**FIGURE 108B**



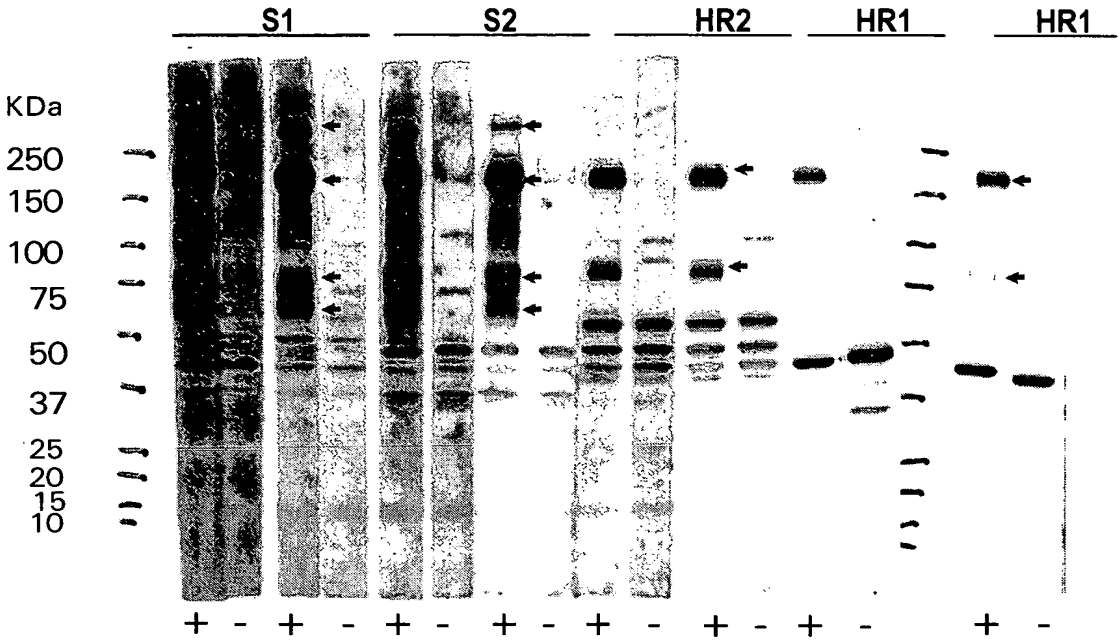
**FIGURE 109**



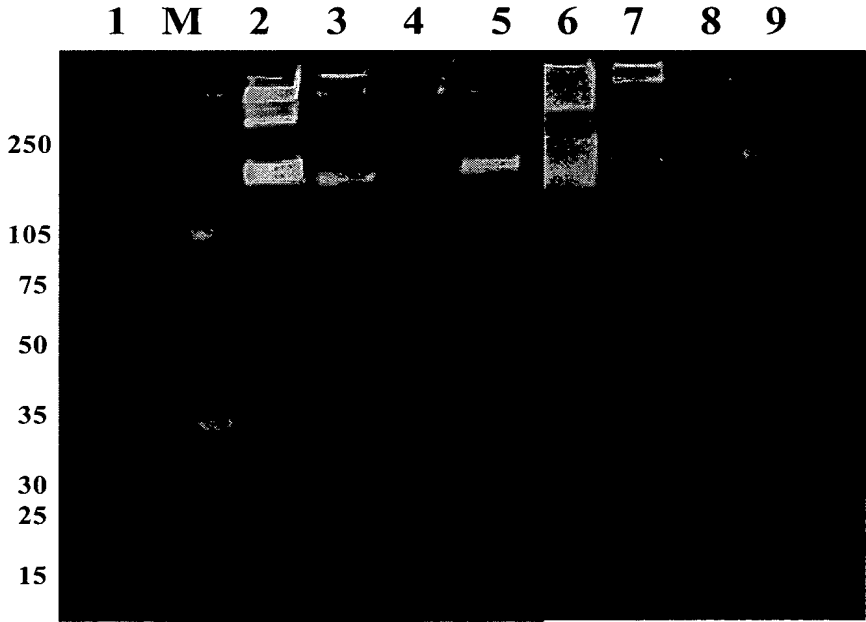
**FIGURE 110**



**FIGURE 111**



**FIGURE 112**



**FIGURE 113****5'3' Frame 1**

PKDMTYVDSSL-WVS-ITKSMVTLICLSPAKKLFVTFVRGLALM-RAVMQLEMLWVLTYLS  
S-DFLQVLT--LYRLVMLTLKITQNSPELMHKPPPVSSSLNILYHSCIKACPGM-CVLR-YK  
CSVIH-KDCQTESCSSFGRMALSLHQ-STLSRLDLKERVVCVTNVQLAFLHQLMPAGII  
LWVLTSITHL-LMFSSGGFTGNLSE-P-PTLPGTWKCTCGLVVML

**5'3' Frame 2**

QRT-PT-THLYDGFQNELPSQWLP-YVYHPRRSYSSRSCVDWL-CRGLSCN-RCCGY-PTS  
PARIFYRC-LSSCTDWLC-H-K-HKIHQS-CTNLHQ-AV-TSYTTHV-RLALECSAY-DST  
NAQ-YTERIVRQSRVRPLGAWL-AYINEVLCQDWT-KNVLSV-QTCNLLFYFIRYLCLLES  
FCGF-LCL-PIYD-CSAVGALRVTFQSNHDQHCQVHGNAHVG-L-C

**5'3' Frame 3**

KGHDLRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPL  
QLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLMYKGLPWNVVRKIVQ  
MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWNH  
SVGFDYVYNPFMIDVQQWGLYG-PFRVTMTNIARYMEMHMMWASCA

**3'5' Frame 1**

-HHN-PTCAFPCTWQCWSWLL-KVTRKAPTAEHQS-MGYRHSQNPQNDSSRHKYLK-KSK  
LHVCHTDNTFFQVQS-QSTSLM-AQSHAPKGRTRLCLTILSVYH-AFVLS-YALHSRASLY  
T-VV-DV-TAHWWRFVH-LW-ILCYFQCQHNQSVQLLS-HL-KILAGEVG-YPQHL-LHDS  
PLHQSQSTHERDE-LLRG--TY-GNH-LGNSF-NPS-R-VYVGHVLW

**3'5' Frame 2**

SITTSPHVHFHVPGNVGHGYSERLPVKPPLLNNHKKWVIDIVKTHRMIPAGISI--SRKAS  
CTFVTQTTRSFRSNLDKVLH-CKLKAMRPKDEHDSV-QSFQCITEHLYYLNTHYIPGQAFI  
HEWYKMFKLLTGGLCINSGEFCVIFSVNITSRYSY-VNTRKS-LER-VSTHSISSCMTA  
LYIKANPRTNVTNSFFAGDKHIRVTIDLVIHFETHHRDEST-VMSF

**3'5' Frame 3**

ASQLAHMCISMYLAMLVMVTLKGYP-SPHC-TSIINGL-T-SKPTE-FQQA-VSDEVEKQV  
ARLSHRQHVLSGPILTKYFIDVSSKPCAQRTNTTSLSDNPFSVLSICTILIRTTFQGKPLY  
MSGIRCLNCSLVEVCALTLVNFVLFVSST-PVGTATKLTPVENPSWRGRLVPTASLVA-QP  
STSKPIHART-RIASSRVINILG-PLTW-FILKPIIEMSLRRSCPL

**FIGURE 114****5'3' Frame 1**

YRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQLGF  
STGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLI

**5'3' Frame 2**

TVDSSL-WVSK-ITKSMVTLICLSPAKKLFVTFVRGLALM-RAVMQLEMLWVLTYLSS-DF  
LQVLT--LYRLVMLTLKITQNSPELMQNLHQVTSLNILY

**5'3' Frame 3**

P-THLYDGFQNELPSQWLP-YVYHPRRSYSSRSCVDWL-CRGLSCN-RCCGY-PTSPARIF  
YRC-LSSCTDWLC-H-K-HRIHQ5-CKTSTR-PV-TSYT

**3'5' Frame 1**

GIRCLNWSPGGGFALTIVNSVLF5VST-PVGTATKLT5VENPSWRGRLVPTASLVA-QPST  
SKPIHART-RIASSRVINILG-PLTW-FILKPIIEMSLR

**3'5' Frame 2**

V-DV-TGHLVEVLH-LW-ILCYFQCQHNQSVQLLS-HL-KILAGEVG-YPQHL-LHDSPLH  
QSQ5THERDE-LLRG--TY-GNH-LGNSF-NPS-R-VYG

**3'5' Frame 3**

YKMFKLVTWWRFCINSGEFCVIFSVNITSRY5Y-VN5TCRKS-LER-VSTHSISSCMTALYI  
KANPRTNVTNSFFAGDKHIRVTIDLVIHFETHHRDESTV

**FIGURE 115**

Section 151

(5851) 5851                      5860                      5870                      5889  
 (5675) LTNYELSVINARIRAKHYVYIGDPAQLPAPRVLLCKGTL  
 (5247) LTNYELSFINGKINYCYVYVVGDPAPLPAPRTLLNG-ST  
 (5762) LTNYELSVINSRVSAKHYVYIGDPAQLPAPRVLLNKGTL  
 (1) -----  
 (5851) LTNYELSVINARI AKHYVYIGDPAQLPAPRVLLNKGTL

Section 152

(5890) 5890                      5900                      5910                      5928  
 (5714) EPKYFNTVTKLMCCCLGPDIFLGTCYRCPKEIVDTVSAIV  
 (5285) SPKDYNVVTNLMVCVKPDIFELAKCYRCPKEIVDTVSTLV  
 (5801) EPRYFNSVTKLMCCCLGPDIFLGTCYRCPKEIVDTVSAIV  
 (1) -----  
 (5890) EPKYFNSVTKLMCCCLGPDIFLGTCYRCPKEIVDTVSAIV

Section 153

(5929) 5929                      5940                      5950                      5967  
 (5753) YENKLKAKNESSSLCFKVYYKG---VTTHESSSAVNMQQ  
 (5324) YDCKFIANNPESRECFKVIHNGNSDVGHESGSAYNTTC  
 (5840) YENKLKAKNDNSSMCFKVYYKG---QTTHESSSAVNMQQ  
 (1) -----  
 (5929) YDNKLKAKND SSLCFKVYYKG                      TTHESSSAVNMQQ

Section 154

(5968) 5968                      5980                      5990                      6006  
 (5789) IYELINKELKANPLWHKAVFISPYNSQNEAAKRVLGLQTO  
 (5363) LEFMKDFVCRNKQWREAFISPYNAMNQRAYRMLGLINVO  
 (5876) IHLISKELKANPSWSNAVFISPYNSQNMVAKRVLGLQTO  
 (1) -----  
 (5968) IHLI KFLKANP W AVFISPYNSQNF AKRVLGLQTO

Section 155

(6007) 6007                      6020                      6030                      6045  
 (5828) TVDSAQGSEYDYVIYSQTAETAHSVNVNRENVAITRAKK  
 (5402) TVDSSQGSEYDYVLECVTADSQHALNENRENVAITRAKK  
 (5915) TVDSAQGSEYDEVYISQTAETAHSVNVNRENVAITRAKK  
 (1) -----  
 (6007) TVDSAQGSEYDYVIYSQTAETAHSVNVNRENVAITRAKK

Section 156

(6046) 6046                      6060                      6070                      → 6084  
 (5867) GILCVMSNMQLFEALOFTTLTLDKMPQAVETRVQCSTNL  
 (5441) GILVVMRQRDELYSALKFTELDSETS-----LQG--TGL  
 (5954) GILCVMSNMQLFESLNFTTLTLDKIN---NPRLOQTTLNL  
 (1) -----  
 (6046) GILCVMSNMQLFESLNFTTLTLDKI                      RLOQSTNL

**START**



**FIGURE 115 (contd.)****Section 157**

(6085) 6085      6090                      6100                      6110                      6123  
 (5906) FKDCSKSYSGYHPAHAPSEFLAVDDKYKATGDLAVCLGIG  
 (5473) FKICNKEESGVHPAYAVTTKALAAATYKVNDELALVNVE  
 (5990) FKDCSRSYVGYHPAHAPSEFLAVDDKYKVGGDLAVCLNVA  
 (1) -----  
 (6085) FKDCSKSYSGYHPAHAPSEFLAVDDKYKV GDLAVCLNVA

**Section 158**

(6124) 6124      6130                      6140                      6150                      6162  
 (5945) D-SAVTYSRLISLMGFRLEDVTLDCYCHLITKEEAVKRV  
 (5512) AGSEITYKHLISLLEFKMSVNVESCHNMFITRDEAIRNV  
 (6029) D-SAVTYSRLISLMGFRLEDVTLDCYCHLITRDEAIRNV  
 (1) --KGHDLRRLISLMGFRMNYQNGYPMNMFITRDEAIRNV  
 (6124) D SAVTYSRLISLMGFKLDVTLDCYCNLFITRDEAIRNV

**Section 159**

(6163) 6163      6170                      6180                      6190                      6201  
 (5983) RAWVGFDAGGAHATRDSIGTNEPLQLGFSTGIDFVVEAT  
 (5551) RGVGFDVEATHACGTNIGTNLPPQVGFSTGADEVVTRE  
 (6067) RAWVGFDAGGAHAIRDSIGTNEPLQLGFSTGIDFVVEAT  
 (38) RAWVGFDVEGCHATRDAVGTTNEPLQLGFSTGMNLVAVET  
 (6163) RAWVGFDVEGAHATRDSIGTNLPLQLGFSTGIDFVVEPT

**Section 160**

(6202) 6202      6210                      6220                      6230                      6240  
 (6022) GLFADRDGYSPKKAVAKAPPGEQFKHLIPLMTRGQRNDV  
 (5590) GLVDTSIGNNEPVMNSKAPPGEQFNHLRVLENSAKPWHV  
 (6106) GMFAERDGYVPKKAAABAPPGEQFKHLIPLMSRGQKWDV  
 (77) GYVDTENNTKETRYNACTSTSEQFKHLIPLMYKGLPWHV  
 (6202) GLVDTRDGY FKKVNAKAPPGEQFKHLIPLMSRGQPWDV

**Section 161**

(6241) 6241      6250                      6260                      6279  
 (6061) VRPRIVQMFADHLIDLSDCVVLTWAANFELTCLRYFAK  
 (5629) VRPRIVQMLADMLCNVSDCVVFVTWCHGLELTTLRYFVK  
 (6145) VRIRIVQMLSDHLADLADSVVLVTWAASFELTCLRYFAK  
 (116) VRIRIVQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVK  
 (6241) VRPRIVQMLADHL DLSDCVVLVTWAHGFELTCLRYFVK

**Section 162**

(6280) 6280      6290                      6300                      6318  
 (6100) VGREISCNVCTKRATAYNSRTGYYGCWRHSVTCLYLYNP  
 (5668) IGKE-OVCSGSRATTENSHTQAYACWKHCHGHEDEVYNP  
 (6184) VGREVCSVCTKRATCENSRTGYYGCWRHSYSCDYLYNP  
 (155) IGPERTCOLCDKRATCFSSSLTYACWNHSGVGFQDYLYNP  
 (6280) IGREISCCVCTKRATCFNSRTGYYACWRHSVGFQDYLYNP

**FIGURE 115 (contd.)**

Section 163				
(6319)	6319	6330	6340	6357
(6139)	LIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTR			
(5706)	LIVDIQQWGYISNLQFNHDLHCNVHGHARVASVDAIMTR			
(6223)	LIVDIQQWGYTESLTSNHDPTCSVHKGAHVASSDAIMTR			
(194)	FMIDVQQWGLYC- PFRVTMTNIARYMEMMMWASCD			
(6319)	LIVDIQQWGYSGSLSSNHDLHCNVHGHARVASVDAIMTR			
Section 164				
(6358)	6358	6370	6380	6396
(6178)	CLAVYDCFCNNENWNVEYPIISNELSENTSCRVLQRVML			
(5745)	CLAVYDCFCNNENWNVEYPIISNELSENTSCRVLQRVML			
(6262)	CLAVYDCFCNNENWNVEYPIISNELSVNTSCRLLQRVML			
(229)	-----			
(6358)	CLAVYDCFCN VWNVEYPIISNELSVNTSCRLLQRVML			
Section 165				
(6397)	6397	6410	6420	6435
(6217)	KAAMLCNRYTLCYDIGNPKAIACVKD--EDEFKFDANPI			
(5784)	NACVDALKVNVVYDIGNPKGIKCVRRGDVNERFYDKNPI			
(6301)	KAAMLCNRYDVCYDIGNPKGLACVKG--YDEFKFDANPI			
(229)	-----			
(6397)	KAAMLCNRY VCYDIGNPKGIACVK EDEFKFDANPI			
Section 166				
(6436)	6436	6450	6460	6474
(6254)	VKSVMKTLTYSEEAHKDSEKDGGLCMFWNCNVDPKYPNAV			
(5823)	VKNVQKQFYDYNOHKDKEADGGLCMFWNCNVDPKYPNAV			
(6338)	VKSVMKQFYKYEAHKDQELDGLCMFWNCNVDPKYPNAV			
(229)	-----			
(6436)	VKSVMKQFLY YEAHKD F DGLCMFWNCNVDPKYP NAV			
Section 167				
(6475)	6475	6480	6490	6500
(6293)	CRFDTRVLN LNLPGCNGGSLYVKNKHAFT PFSRAAFE			
(5862)	CRFDTRVLN LNLPGCNGGSLYVKNKHAFT PFSRAAFE			
(6377)	CRFDTRVLN LNLPGCNGGSLYVKNKHAFT PFSRAAFE			
(229)	-----			
(6475)	CRFDTRVLN LNLPGCNGGSLYVKNKHAFT PFSRAAFE			
Section 168				
(6514)	6514	6520	6530	6540
(6332)	NLKPMPEFFYYSDTPCVYMDGMDAKQVDYVPLKSATCITR			
(5901)	NLKPMPEFFYYSDTPCVYMDGMDAKQVDYVPLKSATCITR			
(6416)	NLKPMPEFFYYSDTPCVYMDGMDAKQVDYVPLKSATCITR			
(229)	-----			
(6514)	NLKPMPEFFYYSDTPCVYMDGMDAKQVDYVPLKSATCITR			

**FIGURE 115 (contd.)**

Section 169				
(6553)	6553	6560	6570	6580 6591
(6371)	CNLGGAVCLKHAE EYREYLESYNTATTAGFTFWVYKTFD			
(5939)	CNLGGAVCKKHAQMYAE E VTSYNAAVTAGFTFWVTNKLH			
(6455)	CNLGGAVCLKHAE EYREYLESYNTATTAGFTFWVYKTFD			
(229)	-----			
(6553)	CNLGGAVCLKHAE EYREYLESYNTATTAGFTFWVYKTFD			
Section 170				
(6592)	6592	6600	6610	6620 6630
(6410)	FYNLWNTFTKLOSLE NVVYNLVKTGHYTGQAGEMPCAII			
(5978)	PYNLWKSEFSALOSIDNTAYNMYKGGHYDAIAGEMPTVIT			
(6494)	FYNLWNTFTRLQSLE NVVYNLVNAGHEDGRAGELPCAII			
(229)	-----			
(6592)	FYNLWNTFTKLOSLE NVVYNLVKAGHYDG AGEMPCAII			
Section 171				
(6631)	6631	6640	6650	6669
(6449)	NDKVYAKIDKEDVVF INNTTPTNVAVELFAKRSIRHH			
(6017)	GDKVFVIDQVEKAVEFVNQTTLPTSVAFELYAKRNIRTL			
(6533)	GEKVFAKIQNE DVVVFKNNTTPTNVAVELFAKRSIRPH			
(229)	-----			
(6631)	GDKVIAKIQ EDVVVF INNTTPTNVAVELFAKRSIR H			
Section 172				
(6670)	6670	6680	6690	6708
(6488)	PELKLFRNLNIDVCWKHV IWDYARESTFCSNTYGVCMYT			
(6056)	PNNRLKGLGV DVTNGFVIWDYANCTPLYRNTVKVCAYT			
(6572)	PELKLFRNLNIDVCWSH VEW DYAKDSVFCSS TYKVCKYT			
(229)	-----			
(6670)	PELKLFRNLNIDVCW HVIWDYAKDSIFCSNTYKVC YT			
Section 173				
(6709)	6709	6720	6730	6747
(6527)	DLKFIDKLVLF DGRDNGALEAFKRSNNGVYISTTKVKS			
(6095)	DLEPNG--LVVLYDDBYGDYQSELAADNAVLVSTQCYKR			
(6611)	DLQCTIESLVLF DGRDNGALEAFKKCRNGVYINTTKIKS			
(229)	-----			
(6709)	DL ID LNVLF DGRDNGALEAFKKA NGVYISTTKIKS			
Section 174				
(6748)	6748	6760	6770	6786
(6566)	LSMIKGPFRALNGVVVDKVGDTDCVFYFAVRKEGODVI			
(6132)	YSYVEIPSNLLVONGMPLKDG-----ANLYV			
(6650)	LSMIKGPQRADLNGVVVEKVGDSDFEFWFAVRKDGNDVI			
(229)	-----			
(6748)	LSMIKGP RADLNGVVVDKVGDSDFWFAVRKDGNDVI			

SEQ ID NO: 10068

SEQ ID NO: 10069

SEQ ID NO: 10070

SEQ ID NO: 9997/98

SEQ ID NO: 10071

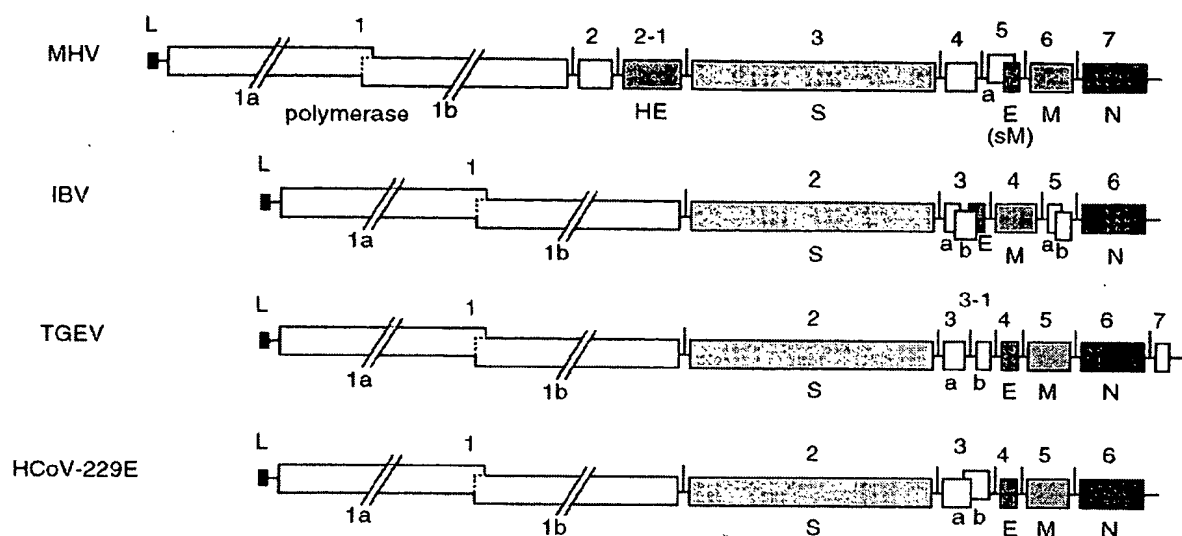
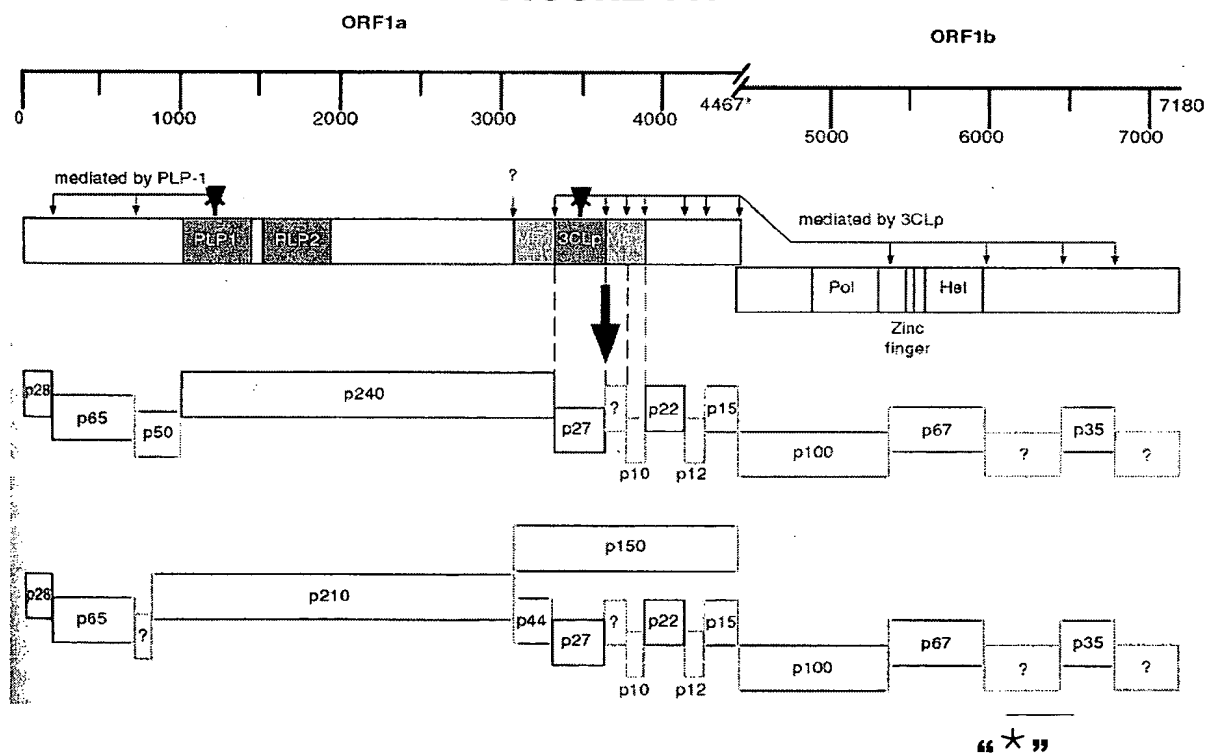
SEQ ID NO: 10068

SEQ ID NO: 10069

SEQ ID NO: 10070

SEQ ID NO: 9997/98

SEQ ID NO: 10071

**FIGURE 116****FIGURE 117**

**FIGURE 118**

Section 1

(1)	1	10	20	30	40	51
(1)	-GTGLFRITNKKEESVTPAYAVETKADAATYKVNDLALVNVEAGKQHDL					
(1)	CSTNLFKDCSKSYSGYHPAHAPSFLAVDDKYKATGDLAVCLDGD-KQHDL					
(1)	CTNLFKDCSRSYVGYHPAHAPSFLAVDDKYKVGCDLAVCLNVAD-KQHDL					
(1)	CSTNLFKDCSKSYSGYHPAHAPSFLAVDDKYKVGCDLAVCLNVAD-KQHDL					
(1)	CSTNLFKDCSKSYSGYHPAHAPSFLAVDDKYKVGCDLAVCLNVAD KQHDL					

Section 2

(52)	52	60	70	80	90	102
(51)	RRLISMGEKMNQVNGYPNMFITREEAIRHVRAWIGEDVEGCHATRDAVG					
(51)	RRLISMGEKMNQVNGYPNMFITREEAIRHVRAWIGEDVEGCHATRDAVG					
(51)	RRLISMGEKMNQVNGYPNMFITREEAIRHVRAWIGEDVEGCHATRDAVG					
(51)	RRLISMGEKMNQVNGYPNMFITREEAIRHVRAWIGEDVEGCHATRDAVG					
(52)	RRLISMGEKMNQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVG					

Section 3

(103)	103	110	120	130	140	153
(102)	TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM					
(102)	TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM					
(102)	TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM					
(102)	TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM					
(103)	TNLPLQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLM					

Section 4

(154)	154	160	170	180	190	204
(153)	YKGLPWNVVRIRKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE					
(153)	YKGLPWNVVRIRKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE					
(153)	YKGLPWNVVRIRKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE					
(153)	YKGLPWNVVRIRKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE					
(154)	YKGLPWNVVRIRKIVQMLSDTLKGLSDRVVFVLWAHGFELTSMKYFVKIGPE					

Section 5

(205)	205	210	220	230	240	255
(204)	RTCCCLCDKRATCFSTSSDTYACWNHSGVEDYVYNPFMIDVQQWGLYGNLQF					
(204)	RTCCCLCDKRATCFSTSSDTYACWNHSGVEDYVYNPFMIDVQQWGLYGSLS					
(204)	RTCCCLCDKRATCFSTSSDTYACWNHSGVEDYVYNPFMIDVQQWGLYGSLS					
(204)	RTCCCLCDKRATCFSTSSDTYACWNHSGVEDYVYNPFMIDVQQWGLYGSLS					
(205)	RTCCCLCDKRATCFSTSSDTYACWNHSGVEDYVYNPFMIDVQQWGLYGSLS					

Section 6

(256)	256	270	280	290	306
(255)	NHDLHCNVHGAHVASVDAIMTRCLAVHDCFCNSVWNWLEYPIISNELSVN				
(255)	NHDLHCNVHGAHVASVDAIMTRCLAVHDCFCNSVWNWLEYPIISNELSVN				
(255)	NHDLHCNVHGAHVASVDAIMTRCLAVHDCFCNSVWNWLEYPIISNELSVN				
(255)	NHDLHCNVHGAHVASVDAIMTRCLAVHDCFCNSVWNWLEYPIISNELSVN				
(256)	NHDLHCNVHGAHVASVDAIMTRCLAVHDCFCNSVWNWLEYPIISNELSVN				

**FIGURE 118 (contd.)**

Section 7

(307) 307	320	330	340	357
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(306) SSCRVLQRMVNLNACMDALKVNVVYDIGNPKGIKCVRRGQDVNFRFYDKNPIV  
 (306) TSCDVLQRMVNLNACMDALKVNVVYDIGNPKGIKCVRRGQDVNFRFYDKNPIV  
 (306) TSCDVLQRMVNLNACMDALKVNVVYDIGNPKGIKCVRRGQDVNFRFYDKNPIV  
 (306) TSCDVLQRMVNLNACMDALKVNVVYDIGNPKGIKCVRRGQDVNFRFYDKNPIV  
 (307) TSCDVLQRMVNLNACMDALKVNVVYDIGNPKGIKCVRRGQDVNFRFYDKNPIV

Section 8

(358) 358	370	380	390	408
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(357) RNVKOEEDYNQHKDKADGLCMFWNCNVDCYFDNSLVCRMDTRNL SVFNL  
 (355) KSVKTLTYSEEAKHDSFKDGLCMFWNCNVDCYFDNSLVCRMDTRNL SVFNL  
 (355) KSVKTLTYSEEAKHDSFKDGLCMFWNCNVDCYFDNSLVCRMDTRNL SVFNL  
 (355) KSVKTLTYSEEAKHDSFKDGLCMFWNCNVDCYFDNSLVCRMDTRNL SVFNL  
 (358) KSVKQFLYSYEAHKDSFKDGLCMFWNCNVDCYFDNSLVCRMDTRNL SVFNL

Section 9

(409) 409	420	430	440	459
-----------	-----	-----	-----	-----

(408) PGCNGGSLYVNHAFHTKPFPSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ  
 (406) PGCNGGSLYVNHAFHTKPFPSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ  
 (406) PGCNGGSLYVNHAFHTKPFPSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ  
 (405) PGCNGGSLYVNHAFHTKPFPSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ  
 (409) PGCNGGSLYVNHAFHTKPFPSRAAFENLKPMPFFFYSDTPCVYMDGMDAKQ

Section 10

(460) 460	470	480	490	500	510
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(458) QDLVSLATKDKITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKT  
 (457) VDYVPLKSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKT  
 (457) VDYVPLKSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKT  
 (456) VDYVPLKSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKT  
 (460) VDYVPLKSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKT

Section 11

(511) 511	524	
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(509) LRPYNLWNTFTKLQ SEQ ID NO: 10073  
 (508) FDFYNLWNTFTKLQ SEQ ID NO: 10074  
 (508) FDFYNLWNTFTKLQ SEQ ID NO: 10075  
 (507) FDFYNLWNTFTKLQ SEQ ID NO: 10076  
 (511) FDFYNLWNTFTKLQ SEQ ID NO: 10077

**FIGURE 119**

tagtcaaaacccacagaatgattccagcaggcataagtatctgatgaagtagaaaagcaa  
 - - - V S D E V E K Q  
 gttgcacgt**TTG**tcacacagacaacacgttctttcaggtccaatc**TTG**acaaagtacttc  
 V A R L S H R Q H V L S G P I L T K Y F  
 attgatgtaagctcaaagccatgcgccccaaaggacgaacacgactctgtctgacaatcct  
 I D V S S K P C A Q R T N T T L S D N P  
 ttcagtgtatcactgagcatttgtactatcttaatacgactacattccagggcaagcct  
 F S V S L S I C T I L I R T T F Q G K P  
 ttatac**ATG**agtggtataagatgtttaaactgctcactgggtggaggtttgtgcattaact  
 L Y M S G I R C L N C S L V E V C A L T  
 Ctggtgaattttgtgttattttcagtggtcaacataa **SEQ ID NO: 10080**  
 L V N F V L F S V S T - **SEQ ID NO: 10027**

**FIGURE 120****FIGURE 120A**

PRHTQRT-PTVDSSL-WVSK-ITKSMVTLICLSPAKKLFVTFVRGLALM-RAVMQL  
 EMLWVLTYLSS-DFLQVLT--LYRLVMLTLKITQNSPELMQNLHQVTSNLILYHSC  
 IKACPGM-CVLR-YKCSVIH-KDCQTESCSSFGRMALSLHQ-STLSRLDLKERVVC  
 VTNVQLAFLHQLMPAGIILWVLTMSITHL-LMFSSGALRVTFRVMTMNIARYME  
 MHMWLVVMLS-LDV-QSMSALLSALIGLLNTLL-EMN-GLILLAKEYNTWL-SLHC  
 LLISFQFFMT-EIQRLSSVCLRLK-NGSSTMLSHVVTKLTK-RNSSILMLYITINS  
 LMVFVCFGIIVTLIVTQPMQLCVGLTQESCQT-TYQAVMVVVC-ISMHSTLQLSIK  
 VHLLI-SNCLSFTILIVLVSLMANK-CRILIMFHSNLLRVLHDAI-VVLFADTMQM  
 STDSTWMHII--FLDLAYGFTNNLILITCGIHLPGYRV

**FIGURE 120B**

LGIPKGHDLP-THLYDGFQNELPSQWLP-YVYHPRRSYSSRSCVDWL-CRGLSCN-  
 RCCGY-PTSPARIFYRC-LSSCTDWLC-H-K-HRIHQS-CKTSTR-PV-TSYTTHV  
 -RLALECSAY-DSTNAQ-YTERIVRQSRVRPLGAWL-AYINEVLCQDWT-KNVLSV  
 -QTCNLLFYFIRYLCLLESFCGF-LCL-PIYD-CSAVGLYG-PSE-P-PTLPGTWK  
 CTCG-L-CYHD-MFSSP-VLC-AR-LVC-IPYYRR-TEG-FCLQKSTTHGCEVCIA  
 C--VSSSS-HRKSKGYQVCASG-SRMEVLRCSAM--QSLQNRGTLLFLCYTSR-IH  
 -WCLFVLEL-R-SLPSQCNCV-V-HKSLVKLELTRL-WW-FVCE-ACIPHSSFR-K  
 CIY-FKAI AFLLLF--SL-VSWQTSSVGY-LCSTQICYVYYTMQFRWCCLQTPCK-  
 VPTVLGCI-YDDFCWI-PMDLQTI-YL-PVEYIYQVTEF

**FIGURE 120C**

-AYPKDMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAV  
 GTNLPLQLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWN  
 VVRIKIVQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFST  
 SSDTYACWNHSGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNHAVASCDAIMTR  
 CLAVHECFVKRVDWSVEYPIIGDELRVNSACRKYQHMVVKSAALLADKFPVLHDIGNPKA  
 IKCVPQAEVEWKFYDAQPCSDKAYKIEELFYSYAIHHDKFTDGVCLFWNCNVDRYPANA  
 IVCRFDTRVLSNLNLPGLDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESH  
 GKQVVSIDIDYVPLKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQF  
 DTYNLWNTFTRLQSL

**FIGURE 120D**

-TL-PGKCIPQVISIKLFVNP-AKSSRNHHIICIQVLSVLICMVSANSTT-IASCNTRS  
 RFEWNIINIRHYLFAMRLTRTIRIVKERQLL-ISKCTFIESWSVECLMHIHQTTTITAW  
 -VQV-QDSCVKPTHNCIGWVTINVTIPKQNTISEFIVMYSIRIEEFLYFVSFVTTWLS  
 IVELPFYFSLRHTLDSLWISYVMKNWKLISKQCRLHNHVLYFSASRINPQFISYNRVFN  
 RPINALNKALMDC-TSSHDSITTSHMCISMYLAMLVMVTLKVTRKAPLLNINHKKWVIDI  
 VKTHRMIPAGISI--SRKASCTFVTQTTRSFRSNLDKVLH-CKLKAMRPKDEHDSV-QS  
 FQCITEHLYLNTHYIPGQAFIHEWYKMFKLVTWWRFCINSGEFCVIFSUNITSRYSY-  
 VNTCRKS-LER-VSTHSISSCMTALYIKANPRTNVTNSFFAGDKHIRVTIDLVIHFETH  
 HRDESTVGHVLWVCL

**FIGURE 120E**

KLCNLVNVFHLR-VSNCL-IHRLNPAEIIILYASKYCRYSAWCLQTAPPKLHRVIHVA  
 DLSGT-SISDTTCLP-DSQGLSE--KKGNCFKLVNALLSKAGVWNAFLTYKLPPSQPG  
 KFKFDKTLVSNLHTIALAG-RSTLQFQNKQTPSVNLS-CIA-E-KSSSIL-ALSLHG-A  
 S-NFHSTSA-GTHLIAFGFPMS-RTGNLSASNADFTTMCCTFLQAEFLTSSSPIIGYST  
 DQSTRLTKHSWTAKHLVMIASQLATCAFPCTWQCWSWLL-RLPVKPHC-TSIINGL-T-  
 SKPTE-FQQA-VSDEVEKQVARLSHRQHVLSPILTKYFIDVSSKPCAQRTNTTSLSDNP  
 FSVLSICTILIRTTFQGKPLYMSGIRCLNWSPGGGFALTLVNSVLFSVST-PVGTATK  
 LTPVENPSWRGRLVPTASLVA-QPSTSKPIHART-RIASSRVINILG-PLTW-FILKPI  
 IEMSLR-VMSFGYA-

**FIGURE 120F**

NSVTW-MYSTGYKYQIVCKSIG-IQQKSSYYMHPSTVGTHLHGVCKQHHLNCIV-YT-Q  
 I-VEHNQYPTLLVCHETHKDYQNSKRKAIALN--MHFYRKLECGMHAYSHTNYHHHSLV  
 SSSLTRLLCQTYTQLHWLGNDQRYNSKTNKHHQ-IYRDV-HKNRRVPLFCKLCHYMAEH  
 RRTSILLQPEAHT--PLDFLCHEELETYQQAMQTSQPCVVLFCKQN-PSVHLL--GIQQ  
 TNQRA-QSTHGLLNI-S--HHN-PHVHFPVPGNVGHGYSEGYP-SPTAEHQ-S-MGYRHS  
 QNPQNDSSSRHKYLMK-KSKLHVCHTDNTFFQVQS-QSTSLM-AQSHAPKGRTRLCLTIL  
 SVYH-AFVLS-YALHSRASLYT-VV-DV-TGHLVEVLH-LW-ILCYFQCQHNQSVQLLS  
 -HL-KILAGEVG-YPQHL-LHDSPLHQSQSTHERDE-LLRG--TY-GNH-LGNSF-NPS  
 -R-VYGRSCPLGMPR



**FIGURE 121**

	10	20	30	40	50	60
SEQ ID NO:10033	-----					TACCGTAGACTCATCTCTATGATGGGTTTCAAAA
SEQ ID NO:10084	CCTAGGCATACCCAAAGGACATGACCTACCGTAGACTCATCTCTATGATGGGTTTCAAAA					
Consensus	TACCGTAGACTCATCTCTATGATGGGTTTCAAAA					
Prim. cons.	CCTAGGCATACCCAAAGGACATGACCTACCGTAGACTCATCTCTATGATGGGTTTCAAAA					
	70	80	90	100	110	120
SEQ ID NO:10033	TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTCCGTC					
SEQ ID NO:10084	TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTCCGTC					
Consensus	TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTCCGTC					
Prim. cons.	TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTCCGTC					
	130	140	150	160	170	180
SEQ ID NO:10033	ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG					
SEQ ID NO:10084	ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG					
Consensus	ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG					
Prim. cons.	ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG					
	190	200	210	220	230	240
SEQ ID NO:10033	GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA					
SEQ ID NO:10084	GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA					
Consensus	GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA					
Prim. cons.	GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA					
	250	260	270	280	290	300
SEQ ID NO:10033	CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC					
SEQ ID NO:10084	CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC					
Consensus	CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC					
Prim. cons.	CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC					
	310	320	330	340	350	360
SEQ ID NO:10033	CAGGTGACCAGTTTAAACATCTTATACC-----					
SEQ ID NO:10084	CAGGTGACCAGTTTAAACATCTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAG					
Consensus	CAGGTGACCAGTTTAAACATCTTATACC					
Prim. cons.	CAGGTGACCAGTTTAAACATCTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAG					

etc.

**FIGURE 122****5'3' Frame 1**

cctaggcatacccaaaggacatgacctaccgtagactcatctctatgatggggtttcaaaa  
 P R H T Q R T - P T V D S S L - W V S K  
 tgaattaccaagtcaatgggttacctaataatgtttatcacccgcgaagaagctattcgtc  
 - I T K S M V T L I C L S P A K K L F V  
 acgttcgtgcgtggattggcctttgatgtagagggtgtcatgcaactagagatgctgtgg  
 T F V R G L A L M - R A V M Q L E M L W  
 gtactaacctacctctccagctaggattttctacagggtgttaacttagtagctgtaccga  
 V L T Y L S S - D F L Q V L T - - L Y R  
 ctgggttatgttgacactgaaaataaacacagaattcaccagagttaatgcaaacctccac  
 L V M L T L K I T Q N S P E L M Q N L H  
 cagggtgaccagtttaaacatcttataaccactcatgtataaaggcttgccctggaatgtag  
 Q V T S L N I L Y H S C I K A C P G M -  
 tgcgtattaagatagtacaaatgctcagtgatacactgaaaggattgtcagacagagtcg  
 C V L R - Y K C S V I H - K D C Q T E S  
 tgttcgtcctttgggcgcgtggcctttgagcttacatcaatgaagtactttgtcaagattg  
 C S S F G R M A L S L H Q - S T L S R L  
 gacctgaaagaacgtgttgctgtgtgacaaacgtgcaacttgcttttctacttcatcag  
 D L K E R V V C V T N V Q L A F L L H Q  
 atacttatgcctgctggaatcattctgtgggttttgactatgtctataacccatttatga  
 I L M P A G I I L W V L T M S I T H L -  
 ttgatgttcagcagtggggctttacgggtaaccttcagagtaaccatgaccaacattgcc  
 L M F S S G A L R V T F R V T M T N I A  
 aggtacatggaaatgcacatgtggctagttgtgatgctatcatgactagatgttttagcag  
 R Y M E M H M W L V V M L S - L D V - Q  
 tccatgagtgctttgttaagcgcgttgattgggtctgttgaaataccctattataggagatg  
 S M S A L L S A L I G L L N T L L - E M  
 aactgagggttaattctgcttgcaaaaagtacaacacatgggtgtgaagtctgcattgc  
 N - G L I L L A E K Y N T W L - S L H C  
 ttgctgataagtttccagttcttcatgacataggaaatccaaaggctatcaagtgtgtgc  
 L L I S F Q F F M T - E I Q R L S S V C  
 ctcaggctgaagtagaatggaagttctacgatgctcagccatgtagtgacaaagcttaca  
 L R L K - N G S S T M L S H V V T K L T  
 aaatagaggaactcttctatttctatgctatacatcacgataaattcactgatgggtgttt  
 K - R N S S I L M L Y I T I N S L M V F  
 gtttggttttggaaattgtaacgttgatcggttaccagccaatgcaattgtgtgtaggtttg  
 V C F G I V T L I V T Q P M Q L C V G L  
 acacaagagtcttgtcaaacttgaacttaccaggctgtgatggtaggtttgtatgtga  
 T Q E S C Q T - T Y Q A V M V V V C M -  
 ataagcatgcattccacactccagctttcgataaaagtgcatttactaatttaaagcaat  
 I S M H S T L Q L S I K V H L L I - S N  
 tgccttttcttttactattctgatagtccttgtgagtcctcatggcaacaagtagtgctgg  
 C L S F T I L I V L V S L M A N K - C R  
 atattgattatgttccactcaaactctgctacgtgtattacacgatgcaatttaggtgggtg  
 I L I M F H S N L L R V L H D A I - V V  
 ctggtttgcagacacccatgcaaatgagtagcagtagtcttggtatgcataataatgatga  
 L F A D T M Q M S T D S T W M H I I - -  
 tttctgctggatttagcctatggattttacaacaatttgataacttataacctgtggaata  
 F L L D L A Y G F T N N L I L I T C G I

catttaccaggttacagagttta  
H L P G Y R V

**5'3' Frame 2**

cctaggcatacccaaaggacatgacctaccgtagactcatctctatgatgggtttcaaaat  
L G I P K G H D L P - T H L Y D G F Q N  
gaattaccaagtcaatgggttaccctaatatgtttatcacccgcgaagaagctattcgta  
E L P S Q W L P - Y V Y H P R R S Y S S  
cgttcgtgctggattggccttgatgtagagggctgtcatgcaactagagatgctgtggg  
R S C V D W L - C R G L S C N - R C C G  
tactaacctacctctccagctaggatgtttctacaggtgttaacttagtagctgtaccgac  
Y - P T S P A R I F Y R C - L S S C T D  
tggttatgttgacactgaaaataacacagaattcaccagaggttaatgcaaaacctccacc  
W L C - H - K - H R I H Q S - C K T S T  
aggtgaccagtttaaacatcttataaccactcatgtataaaggcttgccctggaatgtagt  
R - P V - T S Y T T H V - R L A L E C S  
gcgatattaagatagtacaaatgctcagtgatacactgaaaggattgtcagacagagtcgt  
A Y - D S T N A Q - Y T E R I V R Q S R  
gttcgtcctttgggcgcagtggtttgagcttacatcaatgaagtactttgtcaagattgg  
V R P L G A W L - A Y I N E V L C Q D W  
acctgaaagaacgtgttgctgtgtgacaaacgtgcaacttgcttttctacttcatcaga  
T - K N V L S V - Q T C N L L F Y F I R  
tacttatgcctgctggaatcattctgtgggttttgactatgtctataacccatttatgat  
Y L C L L E S F C G F - L C L - P I Y D  
tgatgttcagcagtggtggcctttacgggtaaccttcagagtaaccatgaccaacattgcc  
- C S A V G L Y G - P S E - P - P T L P  
ggtacatggaaatgcacatgtggctagtgtgtgatgctatcatgactagatgttttagcagt  
G T W K C T C G - L - C Y H D - M F S S  
ccatgagtgctttgttaagcgcgttgattggtctgttgaaataccctattataggagatga  
P - V L C - A R - L V C - I P Y R R -  
actgagggttaattctgcttgagaaaaagtacaacacatgggttggaagtctgcattgct  
T E G - F C L Q K S T T H G C E V C I A  
tgctgataagtttccagttcttcatgacataggaaatccaaaggctatcaagtggtgcc  
C - - V S S S - H R K S K G Y Q V C A  
tcaggctgaagtagaatggaagtctacgatgctcagccatgtagtgacaaagcttaca  
S G - S R M E V L R C S A M - - Q S L Q  
aatagaggaaactcttctattcttatgctatacatcacgataaattcactgatgggtgttg  
N R G T L L F L C Y T S R - I H - W C L  
tttggtttggaattgtaacgcttgatcggttaccagccaatgcaattgtgtgtaggtttga  
F V L E L - R - S L P S Q C N C V - V -  
cacaagagtcctgtcaaaccttgaacttaccaggctgtgatgggtgtagtttgatgtgaa  
H K S L V K L E L T R L - W W - F V C E  
taagcatgcattccacactccagctttcgataaaagtgcatttactaatttaaagcaatt  
- A C I P H S S F R - K C I Y - F K A I  
gcctttcttttactattctgatagtccttgtagtctcatggcaacaagtagtgctcgga  
A F L L L F - - S L - V S W Q T S S V G  
tattgattatgttccactcaaactctgctacgtgtattacacgatgcaatttaggtgggtgc  
Y - L C S T Q I C Y V Y Y T M Q F R W C  
tggttgagacacatgcaaatgagtaccgacagctacttggtatgcatataatatgatgat

C L Q T P C K - V P T V L G C I - Y D D  
 ttctgctggatttagcctatggatttacaaacaatttgatacttataacctgtggaatac  
 F C W I - P M D L Q T I - Y L - P V E Y  
 atttaccaggttacagagttta  
 I Y Q V T E F

**5'3' Frame 3**

cctaggcatacccaaaggacATGacctaccgtagactcatctctatgatgggtttcaaaatg  
 - A Y P K D M T Y R R L I S M M G F K M  
 aattaccaagtcaatggttaccctaataatgtttatcaccgcgaagaagctattcgtcac  
 N Y Q V N G Y P N M F I T R E E A I R H  
 gttcgtgctggattggctttgatgtagagggctgtcatgcaactagagatgctgtgggt  
 V R A W I G F D V E G C H A T R D A V G  
 actaacctacctctccagctaggattttctacaggtgttaacttagtagctgtaccgact  
 T N L P L Q L G F S T G V N L V A V P T  
 gggtatgttgacactgaaaataacacagaattcaccagagttaatgcaaaacctccacca  
 G Y V D T E N N T E F T R V N A K P P P  
 ggtgaccagtttaaacatcttataccactcatgtataaaggcttgccctggaatgtagt  
 G D Q F K H L I P L M Y K G L P W N V V  
 cgtattaagatagtacaaatgctcagtgatacactgaaaggattgtcagacagagtcgtg  
 R I K I V Q M L S D T L K G L S D R V V  
 ttcgtcctttgggcgcagtggtttgagcttacatcaatgaagtactttgtcaagattgga  
 F V L W A H G F E L T S M K Y F V K I G  
 cctgaaagaacgtgttgtctgtgtgacaaacgtgcaacttgcttttctacttcatcagat  
 P E R T C C L C D K R A T C F S T S S D  
 acttatgcctgctggaatcattctgtgggttttgactatgtctataaccatttatgatt  
 T Y A C W N H S V G F D Y V Y N P F M I  
 gatgttcagcagtggggctttacgggtaaccttcagagtaaccatgaccaacattgccag  
 D V Q Q W G F T G N L Q S N H D Q H C Q  
 gtacatggaaatgcacatgtggctagtgtgtatcatgactagatgttttagcagtc  
 V H G N A H V A S C D A I M T R C L A V  
 catgagtgctttgttaagcgcgttgattggtctgttgaaataccctattataggagatgaa  
 H E C F V K R V D W S V E Y P I I G D E  
 ctgagggttaattctgcttgcaaaaagtacaacacatgggttggaagtctgcattgctt  
 L R V N S A C R K V Q H M V V K S A L L  
 gctgataagtttccagttcttcatgacataggaaatccaaaggctatcaagtgtgtgcct  
 A D K F P V L H D I G N P K A I K C V P  
 caggctgaagtagaatggaagtctacgatgctcagccatgtagtgacaaagcttacaaa  
 Q A E V E W K F Y D A Q P C S D K A Y K  
 atagaggaactcttctatttcttatgctatacatcacgataaattcactgatgggtgtttgt  
 I E E L F Y S Y A I H H D K F T D G V C  
 ttgttttggaattgtaacgttgatcggttaccagccaatgcaattgtgtgtaggtttgac  
 L F W N C N V D R Y P A N A I V C R F D  
 acaagagtcttgtcaaacttgaacttaccaggctgtgatgggtgtagttttgtatgtgaat  
 T R V L S N L N L P G C D G G S L Y V N  
 aagcatgcattccacactccagctttcgataaaagtgcatttactaatttaaagcaattg  
 K H A F H T P A F D K S A F T N L K Q L  
 cctttcttttactattctgatagtccttgtgagtcctcatggcaacaagtagtgtcggat  
 P F F Y Y S D S P C E S H G K Q V V S D

attgattatgttccactcaaattctgctacgtgtattacacgatgcaatttaggtggtgct  
 I D Y V P L K S A T C I T R C N L G G A  
 gtttgcagacaccatgcaaattgagtaccgacagtacttggatgcatataatatgatgatt  
 V C R H H A N E Y R Q Y L D A Y N M M I  
 tctgctggatttagcctatggatttacaacaatttgatacttataaacctgtggaataca  
 S A G F S L W I Y K Q F D T Y N L W N T  
 ttaccaggttacagagttta  
 F T R L Q S L

**3'5' Frame 1**

taaactctgtaacctggtaaattgtattccacaggttataagtatcaaattgtttgtaaatt  
 - T L - P G K C I P Q V I S I K L F V N  
 ccataggctaaatccagcagaaatcatcatatttatatgcatccaagtactgtcggctactc  
 P - A K S S R N H H I I C I Q V L S V L  
 atttgcattggtgtctgcaaacagcaccacctaattgcatcgtgtaatacacgtagcaga  
 I C M V S A N S T T - I A S C N T R S R  
 tttgagtggaaacataatcaataatccgacactacttgtttgccatgagactcacaaggact  
 F E W N I I N I R H Y L F A M R L T R T  
 atcagaatagtaaaagaaaggcaattgcttttaaattagtaaatgcacttttatcgaaagc  
 I R I V K E R Q L L - I S K C T F I E S  
 tggagtgtggaatgcatgcttattcacatacaaactaccaccatcacagcctggtaagtt  
 W S V E C M L I H I Q T T T I T A W - V  
 caagtttgacaagactccttgtgtcaaacctacacacaattgcattggctgggtaacgatc  
 Q V - Q D S C V K P T H N C I G W V T I  
 aacgttacaattccaaaacaaacaaacaccatcagtggaatttatcgtgatgtatagcata  
 N V T I P K Q T N T I S E F I V M Y S I  
 agaatagaagagttccttctattttgtaagctttgtcactacatggctgagcatcgtagaa  
 R I E E F L Y F V S F V T T W L S I V E  
 cttccatttctacttcagcctgaggcacacacttgatagcctttggatttccctatgtcatg  
 L P F Y F S L R H T L D S L W I S Y V M  
 aagaactggaaacttatcagcaagcaatgcagacttcacaaccatgtgttgacttttct  
 K N W K L I S K Q C R L H N H V L Y F S  
 gcaagcagaattaacctcagttcatctcctataataggggtattcaacagaccaatcaac  
 A S R I N P Q F I S Y N R V F N R P I N  
 gcgcttaacaaagcactcatggactgctaatacttagtcatgatagcatcacaaactagc  
 A L N K A L M D C - T S S H D S I T T S  
 cacatgtgcatttccatgtacctggcaatgttggtcatggttactctgaagggttaccctg  
 H M C I S M Y L A M L V M V T L K V T R  
 aaagccccactgctgaacatcaatcataaattgggttatagacatagtcaaaacccacaga  
 K A P L L N I N H K W V I D I V K T H R  
 atgattccagcaggcataagtatctgatgaagtagaaaagcaagttgcacgtttgtcaca  
 M I P A G I S I - - S R K A S C T F V T  
 cagacaacacgttctttcaggtccaatcttgacaaagtaacttcattgatgtaagctcaa  
 Q T T R S F R S N L D K V L H - C K L K  
 gccatgcgcccaggaagacgaacacgactctgtctgacaatcctttcagtgatcactgag  
 A M R P K D E H D S V - Q S F Q C I T E  
 catttgtactatcttaatacgcactacattccagggcaagcctttatacatgagtggtat  
 H L Y Y L N T H Y I P G Q A F I H E W Y  
 aagatgtttaaactgggtcacctgggtggaggttttgcattaactctggtgaattctgtggt

K M F K L V T W W R F C I N S G E F C V  
 attttcagtgtcaacataaccagtcggtacagctactaagttaacacctgtagaaaatcc  
 I F S V N I T S R Y S Y - V N T C R K S  
 tagctggagaggttaggttagtaccacagcatctctagttgcatgacagccctctacatc  
 - L E R - V S T H S I S S C M T A L Y I  
 aaagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatattagg  
 K A N P R T N V T N S F F A G D K H I R  
 gtaaccattgacttggttaattcattttgaaacccatcatagagatgagtcctacggtaggt  
 V T I D L V I H F E T H H R D E S T V G  
 catgtcctttgggtatgcctagg  
 H V L W V C L

### 3'5' Frame 2

taaactctgtaacctggtaaattgtattccacaggttataagtatcaaattgtttgtaaattc  
 K L C N L V N V F H R L - V S N C L - I  
 cataggctaaatccagcagaaatcatcatattatgcatccaagtactgtcgggtactca  
 H R L N P A E I I I L Y A S K Y C R Y S  
 tttgcatggtgtctgcaaacagcaccacctaattgcatcgtgtaatacacgtagcagat  
 F A W C L Q T A P P K L H R V I H V A D  
 ttgagtggaaacataatcaatatccgacactacttgtttgccatgagactcacaaggacta  
 L S G T - S I S D T T C L P - D S Q G L  
 tcagaatagtaaaagaaaggcaattgcttttaaattagtaaatgcacttttatcgaaagct  
 S E - - K K G N C F K L V N A L L S K A  
 ggagtgtggaatgcatgcttattcacatacaaactaccaccatcacagcctggtaagttc  
 G V W N A C L F T Y K L P P S Q P G K F  
 aagtttgacaagactcttgtgtcaaacctacacacaattgcattggctgggtaacgatca  
 K F D K T L V S N L H T I A L A G - R S  
 acgtttacaattccaaaacaaacaaacaccatcagtgaaatttatcgatgatagcataa  
 T L Q F Q N K Q T P S V N L S - C I A -  
 gaatagaagagttcctctattttgtaagctttgtcactacatggctgagcatcgtagaac  
 E - K S S S I L - A L S L H G - A S - N  
 ttccattctacttcagcctgaggcacacacttgatagccttttgatttcctatgtcatga  
 F H S T S A - G T H L I A F G F P M S -  
 agaactggaaacttatcagcaagcaatgcagacttcacaacccatgtgttgacttttctg  
 R T G N L S A S N A D F T T M C C T F L  
 caagcagaattaaccctcagttcatctcctataatagggtattcaacagaccaatcaacg  
 Q A E L T L S S S P I I G Y S T D Q S T  
 cgcttaacaaagcactcatggactgctaaacatctagtcatgatagcatcacaactagcc  
 R L T K H S W T A K H L V M I A S Q L A  
 acatgtgcatttccatgtacctggcaatggttggtcatggttactctgaagggttaccgta  
 T C A F P C T W Q C W S W L L - R L P V  
 aagccccactgctgaacatcaatcataaatgggttatagacatagtcaaaacccacagaa  
 K P H C - T S I I N G L - T - S K P T E  
 tgattccagcaggcataagtatctgatgaagtagaaaagcaagttgcacgtttgtcacac  
 - F Q Q A - V S D E V E K Q V A R L S H  
 agacaacacggttcttttcaggtccaatcttgacaaagtacttcattgatgtaagctcaaag  
 R Q H V L S G P I L T K Y F I D V S S K  
 ccatgcgccc aaaggacgaacacgactctgtctgacaatccttttcagtgatcactgagc  
 P C A Q R T N T T L S D N P F S V S L S

atttgactatcttaatacgcactacattccagggaagcctttatacatgagtgggtata  
 I C T I L I R T T F Q G K P L Y M S G I  
 agatgtttaaactggtcacctggtagggttttgcattaactctggtagaattctgtgtta  
 R C L N W S P G G G F A L T L V N S V L  
 ttttcagtgtcaacataaccagtcggtacagctactaagttaacacctgtagaaaatcct  
 F S V S T - P V G T A T K L T P V E N P  
 agctggagaggttaggttagtaccacagcatctctagttgcatgacagccctctacatca  
 S W R G R L V P T A S L V A - Q P S T S  
 aagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatattaggg  
 K P I H A R T - R I A S S R V I N I L G  
 taaccattgacttggtaattcattttgaaacccatcatagagatgagtcctacggtaggtc  
 - P L T W - F I L K P I I E M S L R - V  
 atgtcctttgggtatgcctagg  
 M S F G Y A -

### 3'5' Frame 3

taaactctgtaacctggtaaattgtattccacaggttataagtatcaaattgtttgtaaatcc  
 N S V T W - M Y S T G Y K Y Q I V C K S  
 ataggctaaatccagcagaaatcatcatattatatgcatccaagtactgtcggtagctcat  
 I G - I Q Q K S S Y Y M H P S T V G T H  
 ttgcatggtgtctgcaaacagcaccacctaattgcatcgtgtaatacacgtagcagatt  
 L H G V C K Q H H L N C I V - Y T - Q I  
 tgagtggaaacataatcaatatccgacactacttgtttgccatgagactcacaaggactat  
 - V E H N Q Y P T L L V C H E T H K D Y  
 cagaatagtaaaagaaaggcaattgcttttaaattagtaaatgcactttttatcgaaagctg  
 Q N S K R K A I A L N - - M H F Y R K L  
 gagtgtggaatgcatgcttattcacatacaaactaccaccatcacagcctggtaagttca  
 E C G M H A Y S H T N Y H H S L V S S  
 agtttgacaagactcttgtgtcaaacctacacacaattgcattggctgggtaacgatcaa  
 S L T R L L C Q T Y T Q L H W L G N D Q  
 cgttacaattccaaaacaaacaaacacatcagtgaaatttatcgtgatgtatagcataag  
 R Y N S K T N K H H Q - I Y - R D V - H K  
 aatagaagagttcctctattttgtaagctttgtcactacatggctgagcatcgtagaact  
 N R R V P L F C K L C H Y M A E H R R T  
 tccattctacttcagcctgaggcacacacttgatagcctttggatttcctatgtcatgaa  
 S I L L Q P E A H T - - P L D F L C H E  
 gaactggaaacttatcagcaagcaatgcagacttcacaaccatgtgttgtagcttttctgc  
 E L E T Y Q Q A M Q T S Q P C V V L F C  
 aagcagaattaaccctcagttcatctcctataatagggtattcaacagaccaatcaacgc  
 K Q N - P S V H L L - - G I Q Q T N Q R  
 gcttaacaaagcactcatggactgctaaacatctagtcatgatagcatcacactagcca  
 A - Q S T H G L L N I - S - - H H N - P  
 catgtgcatttccatgtacctggcaatggttgcatggttactctgaagggtaccggtaa  
 H V H F H V P G N V G H G Y S E G Y P -  
 agccccactgctgaacatcaatcataaatgggttatagacatagtcaaaacccacagaat  
 S P T A E H Q S - M G Y R H S Q N P Q N  
 gattccagcaggcataagtatctgatgaagtagaaaagcaagttgcacgtttgtcacaca  
 D S S R H K Y L M K - K S K L H V C H T  
 gacaacacgttcttttcaggtccaatcttgacaaagtacttcattgatgtaagctcaaagc

D N T F F Q V Q S - Q S T S L M - A Q S  
catgcgccc aaaggacgaacacgactctgtctgacaatcctttcagtgtatcactgagca  
H A P K G R T R L C L T I L S V Y H - A  
tttgtactatcttaatacgcactacattccagggcaagcctttatacatgagtggtataa  
F V L S - Y A L H S R A S L Y T - V V -  
gatgtttaaactggtcacctgggtggaggttttgcattaactctggtgaattctgtgttat  
D V - T G H L V E V L H - L W - I L C Y  
tttcagtgtcaacataaccagtcggtacagctactaagttaacacctgtagaaaatccta  
F Q C Q H N Q S V Q L L S - H L - K I L  
gctggagaggttaggttagtaccacagcatctctagttgcatgacagccctctacatcaa  
A G E V G - Y P Q H L - L H D S P L H Q  
agccaatccacgcacgaacgtgacgaatagcttcttcgcggtgataaacatattagggt  
S Q S T H E R D E - L L R G - - T Y - G  
aaccattgacttggttaattcattttgaaacccatcatagagatgagtcctacggtaggtca  
N H - L G N S F - N P S - R - V Y G R S  
tgtcctttgggtatgcctagg  
C P L G M P R



**FIGURE 123**

CCTAGGCATACCCAAAGGACATGACCTACCGTAGACTCATCTCTATGATGGGTTTCAAAATGAATTACCAAGTCAATGGT  
.....i.....N..N.....i.....N....  
TACCCTAATATGTTTATCACCCGCGAAGAAGCTATTCGTACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCA  
.....i.....N.....N.....  
TGCAACTAGAGATGCTGTGGGTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA  
.....N.....  
CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCACCAGGTGACCAGTTTAAACAT  
.....N.....N.....  
CTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAGTGCGTATTAAGATAGTACAAATGCTCAGTGATACACTGAA  
.....N.....N.....N.....  
AGGATTGTCAGACAGAGTCGTGTTTCGTCTTTGGGCGCATGGCTTTGAGCTTACATCAATGAAGTACTTTGTCAAGATTG  
.....N.....N.....  
GACCTGAAAGAACGTGTTGTCTGTGTGACAAACGTGCAACTTGCTTTTCTACTTCATCAGATACTTATGCCTGCTGGAAT  
.....N.....  
CATTCTGTGGGTTTGGTACTATGTCTATAACCCATTTATGATTGATGTTTCAGCAGTGGGGCTTTACGGGTAACCTTCAGAG  
.....N.....N.....N.....  
TAACCATGACCAACATTGCCAGGTACATGGAAATGCACATGTGGCTAGTTGTGATGCTATCATGACTAGATGTTTAGCAG  
.....N.....N.....N.....N.....N.....i.....N.....  
TCCATGAGTGCTTTGTTAAGCGCGTTGATTGGTCTGTTGAATACCCTATTATAGGAGATGAACTGAGGGTTAATTCTGCT  
...N.....N.....  
TGCAGAAAAGTACAACACATGGTTGTGAAGTCTGCATTGCTTGCTGATAAGTTTCCAGTTCTTCATGACATAGGAAATCC  
.....i.....N.....  
AAAGGCTATCAAGTGTGTGCCCTCAGGCTGAAGTAGAATGGAAGTTCTACGATGCTCAGCCATGTAGTGACAAAGCTTACA  
.....N.....N.....N.....  
AAATAGAGGAACTCTTCTATTCTTATGCTATACATCACGATAAATTCAGTGATGGTGTTTGTGTTTGGAAATTGTAAC  
.....N.....N.....  
GTTGATCGTTACCCAGCCAATGCAATTGTGTGTAGGTTTGACACAAGAGTCTTGTCAAACTTGAAGTTACCAGGCTGTGA  
.....N.....N.....  
TGGTGGTAGTTTGTATGTGAATAAGCATGCATTCCACACTCCAGCTTTCGATAAAAGTGCATTTACTAATTTAAAGCAAT  
.....N.....N.....  
TGCCTTTCTTTTACTATTCTGATAGTCCTTGTGAGTCTCATGGCAAACAAGTAGTGTCGGATATTGATTATGTTCCACTC  
.....i.....N.....  
AAATCTGCTACGTGTATTACACGATGCAATTTAGGTGGTGCTGTTTGACAGACACCATGCAAAATGAGTACCGACAGTACTT  
.....N.....N.....N.....  
GGATGCATATAATATGATGATTTCTGCTGGATTTAGCCTATGGATTTACAAACAATTTGATACTTATAACCTGTGGAATA  
..N.....N..N.....N.....  
CATTTACCAGGTTACAGAGTTTA      **SEQ ID NO: 10084**  
.....

**FIGURE 123 (contd.)**

Pos	Score	Pred
21	0.651	Yes
45	0.354	-
48	0.387	-
60	0.590	Yes
76	0.470	-
90	0.676	Yes
145	0.192	-
160	0.410	-
172	0.290	-
247	0.221	-
286	0.219	-
333	0.373	-
355	0.178	-
381	0.286	-
439	0.405	-
459	0.204	-
547	0.289	-
580	0.447	-
597	0.449	-
604	0.290	-
646	0.427	-
667	0.427	-
673	0.208	-
679	0.317	-
694	0.180	-
702	0.554	Yes
710	0.151	-
724	0.384	-
778	0.151	-
819	0.711	Yes
865	0.306	-
917	0.230	-
931	0.214	-
941	0.190	-
985	0.274	-
1012	0.368	-
1060	0.206	-
1120	0.193	-
1135	0.185	-
1147	0.431	-
1240	0.562	Yes
1270	0.377	-
1304	0.190	-
1336	0.353	-
1342	0.312	-
1363	0.213	-
1374	0.178	-
1377	0.096	-
1400	0.056	-

**FIGURE 124**

Sequences:		(bits)
Value		
gi 74827 pir  VFIHJH genome polyprotein 1b - murine hepatit...	638	0.0
gi 14917044 sp P29982 RRPB_CVMJH RNA-directed RNA polymeras...	637	0.0
gi 26007546 ref NP_068668.2  ORF1ab polyprotein [Murine hep...	637	0.0
gi 7769342 gb AAF69332.1 AF208066_2 RNA-directed RNA polyme...	637	0.0
gi 6625761 gb AAF19384.1 AF201929_2 RNA-directed RNA polyme...	637	0.0
gi 2641128 gb AAB86818.1  RNA-directed RNA polymerase [muri...	635	0.0
gi 4377413 emb CAA36202.1  open reading frame 1b (AA 1-2733...	634	0.0
gi 133592 sp P16342 RRPB_CVMA5 RNA-DIRECTED RNA POLYMERASE ...	634	0.0
gi 26008080 ref NP_150073.2  orflab polyprotein [Bovine cor...	633	e-
180		
gi 15077820 gb AAK83365.1  replicase [bovine coronavirus]	633	e-
180		
gi 18033972 gb AAL57305.1  replicase [bovine coronavirus]	633	e-
180		
gi 7769353 gb AAF69342.1 AF208067_2 RNA-directed RNA polyme...	633	e-
180		
gi 17529672 gb AAL40397.1 AF220295_2 RNA polymerase 1b [bov...	623	e-
177		
gi 25121571 ref NP_740618.1  coronavirus nsp11 [Murine hepa...	622	e-
177		
gi 26008092 ref NP_742140.1  coronavirus nsp11 [Bovine coro...	617	e-
175		
gi 10242469 ref NP_066134.1  ORF1ab polyprotein; frameshift...	575	e-
163		
gi 14149033 emb CAC39112.1  replicase polyprotein 1ab [Avia...	575	e-
163		
gi 458735 emb CAA83018.1  potential chimeric protein [Avian...	570	e-
161		
gi 133594 sp P26314 RRPB_IBVB RNA-DIRECTED RNA POLYMERASE (...)	570	e-
161		
gi 29293454 gb AAO67706.1  ORF1b polyprotein [Avian infecti...	565	e-
160		
gi 25121555 ref NP_740631.1  coronavirus nsp11 [Avian infec...	559	e-
158		
gi 9635157 ref NP_058422.1  replicase [Transmissible gastro...	545	e-
153		
gi 19387582 ref NP_598309.1  Pol1 [porcine epidemic diarrhe...	541	e-
152		
gi 12175747 ref NP_073549.1  replicase polyprotein 1ab [Hum...	535	e-
151		
gi 133591 sp P18458 RRPB_BEV RNA-directed RNA polymerase (O...	50	8e-
05		
gi 1513061 dbj BAA13323.1  cyanoprotein alpha subunit precu...	35	3.7

## Alignments

>gi|74827|pir||VFIHJH genome polyprotein 1b - murine hepatitis virus  
(strain JHM)

Length = 2731

Score = 638 bits (1645), Expect = 0.0  
 Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPLQ 65  
 +TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HATRD++GTN PLQ  
 Sbjct: 1585 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHATRDSIGTNFPLQ  
 1644

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
 LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ  
 Sbjct: 1645 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLVPLMSRGQKWDVVRIRIVQ  
 1704

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185  
 MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW  
 Sbjct: 1705 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVVCVSNKRATCFNSRTGYGVCWR  
 1764

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245  
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K  
 Sbjct: 1765 HSYSCDYLYNPLIVDIQQWGYTGS LTSNHD PICSVHKGAHVASSDAIMTRCLAVHDCFK  
 1824

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305  
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++  
 Sbjct: 1825 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF  
 1882

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365  
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVLS  
 Sbjct: 1883 KFYDASPV---VKS VKQFVYKYEAKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLSK  
 1939

Query: 366 LNLPGCDGGS LYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVS DIDIYVPL 425  
 LNLPGC+GGS LYVNKHAFHT F ++AF NLK +PFFYYSD+PC +D YVPL  
 Sbjct: 1940 LNLPGCNGGS LYVNKHAFHTNPFTAAAFENLKPMFPFFYYSDTPCVYMEGMESKQVDYVPL  
 1999

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDYTNLWNTFTRLQS 485  
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS  
 Sbjct: 2000 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS  
 2059

Query: 486 L 486  
 L  
 Sbjct: 2060 L 2060

>gi|14917044|sp|P29982|RRPB\_CVMJH RNA-directed RNA polymerase (ORF1B)  
 gi|7583321|gb|AAA46458.2| open reading frame 1b [murine hepatitis virus]  
 Length = 2731

Score = 637 bits (1644), Expect = 0.0  
 Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPLQ 65  
 +TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HATRD++GTN PLQ  
 Sbjct: 1585 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHAHATRDSIGTNFPLQ  
 1644

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
 LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ  
 Sbjct: 1645 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLVPLMSRGQKWDVVRIRIVQ  
 1704

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185  
 MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW  
 Sbjct: 1705 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVVCVCNKRATCFNSRTGGYGCWR  
 1764

Query: 186 HSVGFDYVYNPFMIDVQWQWGTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245  
 HS DY+YNP ++D+QWQW+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K  
 Sbjct: 1765 HSYSCDYLYNPLIVDIQWQGYTGSLSNHDPICSVHKGAVASSDAIMTRCLAVHDCFCK  
 1824

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305  
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++  
 Sbjct: 1825 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF  
 1882

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365  
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVLS  
 Sbjct: 1883 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDKYPANAVVCRFDTRVLSK  
 1939

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425  
 LNLPGC+GGSLYVNKHAFT F ++AF NLK +PFFYYSD+PC +DYVPL  
 Sbjct: 1940 LNLPGCNGGSLYVNKHAFTNPFTRAAFENLKPMPPFFYYSDTPCVMEGMESKQVDYVPL  
 1999

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485  
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS  
 Sbjct: 2000 RSATCITRCNLGGAVCLKHAEEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS  
 2059

Query: 486 L 486  
 L  
 Sbjct: 2060 L 2060

>gi|26007546|ref|NP\_068668.2| ORFlab polyprotein [Murine hepatitis virus]  
 Length = 7178

Score = 637 bits (1644), Expect = 0.0  
 Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPLQ 65  
 +TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ  
 Sbjct: 6032 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHAIRDSIGTNFPLQ  
 6091

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
 LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ  
 Sbjct: 6092 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ  
 6151

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185  
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW  
 Sbjct: 6152 MLSDHLADLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGGYGCWR  
 6211

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245  
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K  
 Sbjct: 6212 HSYSCDYLYNPLIVDIQQWGYTGSLTSNHDPICSVHKGAVASSDAIMTRCLAVHDCFK  
 6271

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305  
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++  
 Sbjct: 6272 SVNWNLEYPIISNEVSVNTSCRLLQRMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF  
 6329

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLNS 365  
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+  
 Sbjct: 6330 KFYDASPV---VKSVMQFVYKYEAHKDQFLDGLCMFWNCNVDKYPANAVVCRFDTRVLNK  
 6386

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425  
 LNLPGC+GGSLYVNKHAFT F ++AF NLK +PFFYYSD+PC +DYVPL  
 Sbjct: 6387 LNLPGCNGGSLYVNKHAFTSPFTRA AFENLKPMPPFFYYSDTPCVYMEGMESKQVDYVPL  
 6446

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485  
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS  
 Sbjct: 6447 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS  
 6506

Query: 486 L 486  
 L  
 Sbjct: 6507 L 6507

>gi|7769342|gb|AAF69332.1|AF208066\_2 RNA-directed RNA polymerase [murine  
 hepatitis virus]  
 Length = 2732

Score = 637 bits (1644), Expect = 0.0  
 Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLPLQ 65  
 +TY RLIS+MGFK++ ++GY +FITR+EAIR VRAW+GFD EG HATRD++GTN PLQ  
 Sbjct: 1586 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIRRVRAWVGFDAEGAHATRDSIGTNFPLQ  
 1645

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
 LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ

Sbjct: 1646 LGFSTGIDFVVEATGMFAERDGYVFKKAVARAPPGEQFKHLVPLMSRGQKWDVVRIIRIVQ  
1705

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185  
MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW

Sbjct: 1706 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVVCVNCNKRATCFNSRTGYGWCWR  
1765

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245  
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1766 HSYSCDYLYNPLIVDIQQWGYTGSLTSNHDLICSVHKGAVASSDAIMTRCLAVHDCFCCK  
1825

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305  
V+WS+EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++

Sbjct: 1826 SVNWSLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF  
1883

Query: 306 KFYDAQPCSDKAYKIEELFYSYAIHHDKFTDGVCLFWNCNVDYRYPANAIVCRFDTRVLSN 365  
KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+

Sbjct: 1884 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDKYPANAVCRFDTRVLNK  
1940

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVSDIDYVPL 425  
LNLPGC+GGSLYVNKHAFT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1941 LNLPGCNGGSLYVNKHAFTSPFTRA AFENLKPMFPFFYYSDTPCVYMEGMESKQVDYVPL  
2000

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDYTNLWNTFTRLQS 485  
+SATCITRCNLGGAVC HA +YR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

Sbjct: 2001 RSATCITRCNLGGAVCLKHAEDYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS  
2060

Query: 486 L 486  
L

Sbjct: 2061 L 2061

>gi|6625761|gb|AAF19384.1|AF201929\_2 RNA-directed RNA polymerase [murine  
hepatitis virus strain 2]

gi|7739595|gb|AAF68920.1|AF207902\_2 RNA-directed RNA polymerase [murine  
hepatitis virus strain ML-11]

Length = 2733

Score = 637 bits (1643), Expect = 0.0

Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLPLQ 65  
+TY RLIS+MGFK++ ++GY +FITR+EAIR VRAW+GFD EG HATRD++GTN PLQ

Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIRRVRAWVGFD AEGAHATRDSIGTNFPLQ  
1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ

Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKKAVARAPPGEQFKHLVPLMSRGQKWDVVRIIRIVQ  
1706

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185  
MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW

Sbjct: 1707 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVVCVKNRATCFNSRTGGYGCWR  
1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNHVASCDAIMTRCLAVHECFVK 245  
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLSNHDLCVHKGAVHASSDAIMTRCLAVHDCFCCK  
1826

Query: 246 RVDWSVEYPIIGDELRVNSACRQVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305  
V+WS+EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++

Sbjct: 1827 SVNWSLEYPIISNEVSVNTSCRLLQRMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF  
1884

Query: 306 KFYDAQPCSDKAYKIEELFYSYAIHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365  
KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+

Sbjct: 1885 KFYDASPV--VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDKYPANAVCRFDTRVLNK  
1941

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425  
LNLPGC+GGSLYVNKHAFT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1942 LNLPGCNGGSLYVNKHAFTSPFTRAFAENLKPMPPFFYYSDTPCVYMEGMESKQVDYVPL  
2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485  
+SATCITRCNLGGAVC HA +YR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

Sbjct: 2002 RSATCITRCNLGGAVCLKHAEDYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS  
2061

Query: 486 L 486  
L

Sbjct: 2062 L 2062

>gi|2641128|gb|AAB86818.1| RNA-directed RNA polymerase [murine hepatitis  
virus]

Length = 2733

Score = 635 bits (1637), Expect = 0.0

Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPLQ 65  
+TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ

Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAGAHAIKDSIGTNFPLQ  
1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ

Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRGQKWDVVRIIRIVQ  
1706



Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185  
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW  
 Sbjct: 1707 MLSDHLADLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGGYGCWR  
 1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245  
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K  
 Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLSNHDPICSVHKGAVASSDAIMTRCLAVHDCFCK  
 1826

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKSALLADKFPVLHDIGNPKAIKCVPAEVEW 305  
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++  
 Sbjct: 1827 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF  
 1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365  
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+  
 Sbjct: 1885 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK  
 1941

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVSDIDYVPL 425  
 LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL  
 Sbjct: 1942 LNLPGCNGGSLYVNKHAFHTSPFTRA AFENLKPMPFFYYSDTPCVMEGMESKQVDYVPL  
 2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485  
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS  
 Sbjct: 2002 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS  
 2061

Query: 486 L 486  
 L  
 Sbjct: 2062 L 2062

>gi|4377413|emb|CAA36202.1| open reading frame 1b (AA 1-2733) [Murine  
 hepatitis virus]  
 Length = 2733

Score = 634 bits (1636), Expect = 0.0  
 Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPLQ 65  
 +TY RLIS+MGFK++ ++GY +FTR+EAI+ VRAW+GFD EG HA RD++GTN PLQ  
 Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHAIRDSIGTNFPLQ  
 1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
 LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ  
 Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRQKWDVVRIVQ  
 1706

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185  
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW

Sbjct: 1707 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYGWCWR  
1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245  
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFCK  
1826

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305  
V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++

Sbjct: 1827 SVNWNLEYPIISNEVSVNTSRLQLQRMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF  
1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365  
KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+

Sbjct: 1885 KFYDASPV--VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDPKYPANAVVCRFDTRVLNK  
1941

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVPL 425  
LNLPGC+GGSLYVNKHAFT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1942 LNLPGCNGGSLYVNKHAFTSPFTRAAFENLKPMFPFFYYSDTPCVMEGMESKQVDYVPL  
2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485  
+SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

Sbjct: 2002 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS  
2061

Query: 486 L 486  
L

Sbjct: 2062 L 2062

>gi|133592|sp|P16342|RRPB\_CVMA5 RNA-DIRECTED RNA POLYMERASE (ORF1B)  
gi|93916|pir||S15760 genome polyprotein - murine hepatitis virus (strain  
A59)

Length = 2733

Score = 634 bits (1636), Expect = 0.0

Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPLQ 65  
+TY RLIS+MGFK++ ++GY +FTR+EAI+ VRAW+GFD EG HA RD++GTN PLQ

Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAGAHAIKDSIGTNFPLQ  
1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ

Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKAAARAPPGEQFKHLIPLMSRQKWDVVRIRIVQ  
1706

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185  
MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW

Sbjct: 1707 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYGWCWR  
1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245  
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K  
 Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLTSNHDPICSVHKGAVASSDAIMTRCLAVHDCFCK  
 1826

Query: 246 RVDWSVEYPIIGDELRVNSACRQVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305  
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++  
 Sbjct: 1827 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF  
 1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365  
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+  
 Sbjct: 1885 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDPYANAVVCRFDTRVLNK  
 1941

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425  
 LNLPGC+GGSLYVNKHAFT F ++AF NLK +PFFYYSD+PC +DYVPL  
 Sbjct: 1942 LNLPGCNGGSLYVNKHAFTSPFTRAAFENLKPMPPFFYYSDTPCVMEGMESKQVDYVPL  
 2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485  
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS  
 Sbjct: 2002 RSATCITRCNLGGAVCLKHAEEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS  
 2061

Query: 486 L 486  
 L  
 Sbjct: 2062 L 2062

>gi|26008080|ref|NP\_150073.2| orflab polyprotein [Bovine coronavirus]  
 Length = 7094

Score = 633 bits (1633), Expect = e-180  
 Identities = 284/481 (59%), Positives = 367/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPLQ 65  
 +TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ  
 Sbjct: 5948 VTYSRLISLMGFKLDVTLDDGYCKLFITKEEAVKRVRWVGFDAGAHATRDSIGTNFPLQ  
 6007

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
 LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ  
 Sbjct: 6008 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ  
 6067

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185  
 M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW  
 Sbjct: 6068 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGYGWCWR  
 6127

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245  
 HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF

Sbjct: 6128 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVYDCFCN  
6187

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKALLADKFPVLHDIGNPKAIKCVPAEVEW 305  
++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++

Sbjct: 6188 NINWNVEYPIISNELSINTSCRVLQRVMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF  
6245

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365  
KFYDAQP ++ L YS+ H D F DG+C+FWNCNVD+YP NA+VCRFDTRVL+N

Sbjct: 6246 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDKYPPNAVVCRFDTVLNN  
6302

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425  
LNLPGC+GGSLYVNKHAFHT F ++AF +LK +PFFYYSD+PC +DYVPL

Sbjct: 6303 LNLPGCNGGSLYVNKHAFHTKPFSSRAAFEHLKPMPPFFYYSDTPCVYMDGMDAKQVDYVPL  
6362

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485  
KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQS

Sbjct: 6363 KSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQS  
6422

Query: 486 L 486

L

Sbjct: 6423 L 6423

>gi|15077820|gb|AAK83365.1| replicase [bovine coronavirus]  
Length = 7094

Score = 633 bits (1633), Expect = e-180

Identities = 284/481 (59%), Positives = 367/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLPLQ 65  
+TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ

Sbjct: 5948 VTYSRLISLMGFKLDVTLDDGYCKLFITKEEAVKRVRWVGFDAGAHATRDSIGTNFPLQ  
6007

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ

Sbjct: 6008 LGFSTGIDFVVEATGLFADR DGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ  
6067

Query: 126 MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185  
M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW

Sbjct: 6068 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGYGCWR  
6127

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245  
HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF

Sbjct: 6128 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVYDCFCN  
6187

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKALLADKFPVLHDIGNPKAIKCVPAEVEW 305

++W+VEYPPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++  
 Sbjct: 6188 NINWNVEYPPIISNELSINTSCRVLQVRMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF  
 6245

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365  
 KFYDAQP ++ L YS+ H D F DG+C+FWNCNVD+YP NA+VCRFDTRVL+N

Sbjct: 6246 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDKYPPNAVCRFDTRVLNN  
 6302

Query: 366 LNLPGCDGGS LYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVS DIDIYVPL 425  
 LNLPGC+GGS LYVNKHAFT F ++AF +LK +PFFYYSD+PC +DYVPL

Sbjct: 6303 LNLPGCNGGS LYVNKHAFTKPF SRAAFEHLKPM PFFYYSDTPCVYMDGMDAKQVDYVPL  
 6362

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485  
 KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQS

Sbjct: 6363 KSATCITRCNLGGAVCLKHAEEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQS  
 6422

Query: 486 L 486

L

Sbjct: 6423 L 6423

>gi|18033972|gb|AAL57305.1| replicase [bovine coronavirus]  
 Length = 7094

Score = 633 bits (1633), Expect = e-180

Identities = 284/481 (59%), Positives = 367/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISM MGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPLQ 65  
 +TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ

Sbjct: 5948 VTYSRLISLMGFKLDVTL DGYCKLFITKEEAVKRVRWVGFD AEGAHATRDSIGTNFPLQ  
 6007

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
 LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ

Sbjct: 6008 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ  
 6067

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185  
 M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW

Sbjct: 6068 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGYGCWR  
 6127

Query: 186 HSVGF DYVYNPF MIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCD AIMTRCLAVHECFVK 245  
 HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF

Sbjct: 6128 HSVTC DYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVDCFCN  
 6187

Query: 246 RVDWSVEYPPIIGDEL RVNSACRKVQH MVVKSALLADKFPVLHDIGNPKAIKVPQAEVEW 305  
 ++W+VEYPPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++

Sbjct: 6188 NINWNVEYPPIISNELSINTSCRVLQVRMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF  
 6245

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365  
 KFYDAQP ++ L YS+ H D F DG+C+FWNCNVD+YP NA+VCRFDTRVL+N  
 Sbjct: 6246 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDPKPPNAVVCRFDTRVLNN  
 6302

Query: 366 LNLPGCDGGS LYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDIDYVPL 425  
 LNLPGC+GGS LYVNKHAFT F ++AF +LK +PFFYYSD+PC +DYVPL  
 Sbjct: 6303 LNLPGCNGGS LYVNKHAFTKPF SRAAFEHLKPM PFFYYSDTPCVYMDGMDAKQVDYVPL  
 6362

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485  
 KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQS  
 Sbjct: 6363 KSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQS  
 6422

Query: 486 L 486  
 L  
 Sbjct: 6423 L 6423

>gi|7769353|gb|AAF69342.1|AF208067\_2 RNA-directed RNA polymerase [murine  
 hepatitis virus]  
 Length = 2733

Score = 633 bits (1633), Expect = e-180  
 Identities = 285/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRRLISMGMFYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLPLQ 65  
 ++Y RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ  
 Sbjct: 1587 VSYRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFD AEGAHAIRDSIGTNFPLQ  
 1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
 LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ  
 Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRQKWDVVRIRIVQ  
 1706

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185  
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW  
 Sbjct: 1707 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYG CWR  
 1766

Query: 186 HSVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245  
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K  
 Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGS LTSNHD PICSVHKGAHVASSDAIMTRCLAVHDCFK  
 1826

Query: 246 RVDWSVEYPIIGDEL RVNSACRKVQHMVVK SALLADKFPVLHDIGNPKAIKCVPAEVEW 305  
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++  
 Sbjct: 1827 SVNWNLEYPIISNEVSVNTSRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF  
 1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365  
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+

Sbjct: 1885 KFYDASPV---VKS VKQFVYKYEAHKDQFLDGLCMFWNCNVDKYPANAVVCRFDTRVLNK  
1941

Query: 366 LNLPGCDGGS LYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVS DIDIYVPL 425  
LNLPGC+GGS LYVNKHAFT F ++AF NLK +PFFYYSD+PC +D YVPL

Sbjct: 1942 LNLPGCNGGS LYVNKHAFTSPFTRA AFENLKPM PFFYYSDTPCVMEGMESKQVDYVPL  
2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485  
+SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

Sbjct: 2002 RSATCITRCNLGGAVCLKHAEEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS  
2061

Query: 486 L 486  
L

Sbjct: 2062 L 2062

>gi|17529672|gb|AAL40397.1|AF220295\_2 RNA polymerase 1b [bovine  
coronavirus]

Length = 2685

Score = 623 bits (1607), Expect = e-177

Identities = 282/481 (58%), Positives = 365/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65  
+TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ

Sbjct: 1574 VTYSRLISLMGFKLDVTL DGYCKLFITKEEAVKRVRRAWVGFDAEGA HATRDSIGTNFPLQ  
1633

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ

Sbjct: 1634 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ  
1693

Query: 126 MLSDTLKGLSDRVV FVLWAHGFE LTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185  
M +D L LSD VV V WA FELT ++YF K+G E +C + KRAT +++ + Y CW

Sbjct: 1694 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVSTKRATAYNSRTGYG CWR  
1753

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245  
HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF

Sbjct: 1754 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVYDCFCN  
1813

Query: 246 RVDWSVEYPIIGDEL RVNSACRKVQH MVVKSALLADKFPVLHDIGNPKAIKCVPAEVEW 305  
++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++

Sbjct: 1814 NINWNVEYPIISNELSINTSCRVLQRV MLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF  
1871

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365  
KFYDAQP ++ L Y + H D F DG+C+FWNCNV D+YP NA+VCRFDTRVL+N

Sbjct: 1872 KFYDAQPI---VKS VKTLLYFFEAHKDSFKDGLCMFWNCNVDKYPPNAV VCRFDTRVLNN  
1928

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVSDIDYVPL 425  
 LNLPGC+GGSLYVNKHAFT F ++AF +LK +PFFYYSD+PC +DYVPL  
 Sbjct: 1929 LNLPGCNGGSLYVNKHAFTKPFSSRAAFEHLKPMPPFFYYSDTPCVYMDGMDAQVDYVPL  
 1988

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485  
 KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQS  
 Sbjct: 1989 KSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQS  
 2048

Query: 486 L 486  
 L  
 Sbjct: 2049 L 2049

>gi|25121571|ref|NP\_740618.1| coronavirus nsp11 [Murine hepatitis virus]  
 Length = 521

Score = 622 bits (1603), Expect = e-177  
 Identities = 284/479 (59%), Positives = 362/479 (75%), Gaps = 5/479 (1%)

Query: 6 MTYRRLLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65  
 +TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ  
 Sbjct: 48 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAGAHAIIRDSIGTNFPLQ 107

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
 LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ  
 Sbjct: 108 LGFSTGIDFVVEATGMFAERDGYVFKAAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ 167

Query: 126 MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDYACWN 185  
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW  
 Sbjct: 168 MLSDHLADLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYGVCWR 227

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245  
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K  
 Sbjct: 228 HSYSCDYLYNPLIVDIQQWGYTGSLSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFK 287

Query: 246 RVDWSVEYPIIGDELRVNSACRKYQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVEW 305  
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++  
 Sbjct: 288 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 345

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365  
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVDRYPANA+VCRFDTRVL+  
 Sbjct: 346 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK 402

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVSDIDYVPL 425  
 LNLPGC+GGSLYVNKHAFT F ++AF NLK +PFFYYSD+PC +DYVPL  
 Sbjct: 403 LNLPGCNGGSLYVNKHAFTSPFTRAFFENLKPMPPFFYYSDTPCVYMEGMESKQVDYVPL 462

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484  
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQ  
 Sbjct: 463 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQ 521

>gi|26008092|ref|NP\_742140.1| coronavirus nsp11 [Bovine coronavirus]



Length = 521

Score = 617 bits (1590), Expect = e-175

Identities = 282/479 (58%), Positives = 365/479 (76%), Gaps = 5/479 (1%)

Query: 6 MTYRRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRRAWIGFDVEGCHATRDAVGTNLPLQ 65  
 +TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ  
 Sbjct: 48 VTYSRLISLMGFKLDVTLDDGYCKLFITKEEAVKRVRAWVGFDAGAHATRDSIGTNFPLQ 107

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125  
 LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ  
 Sbjct: 108 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ 167

Query: 126 MLSDTLKGLSDRVVFWLWAGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185  
 M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW  
 Sbjct: 168 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGYGWCWR 227

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245  
 HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF  
 Sbjct: 228 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVYDCFCN 287

Query: 246 RVDWSVEYPIIGDELRVNSACRQVQHMVVSALLADKFPVLHDIGNPKAIKCVPAEVEW 305  
 ++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++  
 Sbjct: 288 NINWNVEYPIISNELSINTSCRVLQRVMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF 345

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCFLWNCNVDYRYPANAIVCRFDTRVLSN 365  
 KFYDAQP ++ L YS+ H D F DG+C+FWNCNVD+YP NA+VCRFDTRVL+N  
 Sbjct: 346 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDKYPPNAVCRFDTRVLNN 402

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425  
 LNLPGC+GGSLYVNKHAFHT F ++AF +LK +PFFYYSD+PC +DYVPL  
 Sbjct: 403 LNLPGCNGGSLYVNKHAFHTKPFSSRAAFEHLKPMPPFFYYSDTPCVYMDGMDAKQVDYVPL 462

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484  
 KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQ  
 Sbjct: 463 KSATCITRCNLGGAVCLKHAEEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQ 521

>gi|10242469|ref|NP\_066134.1| ORFlab polyprotein; frameshift product  
 [Avian infectious bronchitis  
 virus]

Length = 6629

Score = 575 bits (1482), Expect = e-163

Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRRAWIGFDVEGCHATRDAVGTNLPL 64  
 ++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP  
 Sbjct: 5515 EITYKHLISLLGFKMSVNVGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPF  
 5574

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 124  
 Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV  
 Sbjct: 5575 QVGSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAPKWHVIRPRIV  
 5634

Query: 125 QMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACW 184  
 QML+D L +SD VVFFV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW  
 Sbjct: 5635 QMLADNLCNVSDCVVFTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSTQAYACW  
 5693

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244  
 H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DAIMTRCLA++ F  
 Sbjct: 5694 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAVASVDAIMTRCLAINNAFC  
 5753

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVE 304  
 + V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V  
 Sbjct: 5754 QDVNWDLTYPHIANEDEVNSSCRYLQRMVNLACVDALKVNVVYDIGNPKGIKCVRRGDVN  
 5813

Query: 305 WKFYDAQPCSDKAYKIEELFYSYAIHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364  
 ++FYD P + E Y Y H DKF DG+C+FWNCNVDP YP N++VCR+DTR LS  
 Sbjct: 5814 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNLVCRYDTRNLS  
 5870

Query: 365 NLNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVP 424  
 NLPGC+GGSLYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V  
 Sbjct: 5871 VFNLPGCNGGSLYVNKHAFYTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS  
 5929

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484  
 L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ  
 Sbjct: 5930 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ  
 5989

Query: 485 SL 486  
 S+  
 Sbjct: 5990 SI 5991

>gi|14149033|emb|CAC39112.1| replicase polyprotein lab [Avian infectious  
 bronchitis virus (strain  
 Beaudette CK)]  
 Length = 6629

Score = 575 bits (1482), Expect = e-163  
 Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPL 64  
 ++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP  
 Sbjct: 5515 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPL  
 5574

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIV 124  
 Q+GFASTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV  
 Sbjct: 5575 QVGFASTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV  
 5634

Query: 125 QMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACW 184

QML+D L +SD VV FV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW  
 Sbjct: 5635 QMLADNLCNVSDCVVFWTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW  
 5693

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244  
 H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DAIMTRCLA++ F  
 Sbjct: 5694 KHCLGFDVYNPLLVDIQWGYSGNLQFNHDLHCNVHGHAHVASVDAIMTRCLAINNAFC  
 5753

Query: 245 KRVDWSVEYPIIGDELRVNSACRKYQHMVKSALLADKFPVLHDIGNPKAICKVPQAEVE 304  
 + V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V  
 Sbjct: 5754 QDVNWDLTYPHIANEDEVNSSCRYLQRMVNLACVDALKVNVVVDIGNPKGIKCVRRGDVN  
 5813

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364  
 ++FYD P + E Y Y H DKF DG+C+FWNCNVD YP N++VCR+DTR LS  
 Sbjct: 5814 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNSLVCRYDTRNLS  
 5870

Query: 365 NLNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDIDYVP 424  
 NLPGC+GGSLYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V  
 Sbjct: 5871 VFNLPGCNGGSLYVNKHAFYTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS  
 5929

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484  
 L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ  
 Sbjct: 5930 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ  
 5989

Query: 485 SL 486  
 S+  
 Sbjct: 5990 SI 5991

>gi|458735|emb|CAA83018.1| potential chimeric protein [Avian infectious  
 bronchitis virus]  
 Length = 2155

Score = 570 bits (1470), Expect = e-161  
 Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPL 64  
 ++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP  
 Sbjct: 1596 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPL  
 1655

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIV 124  
 Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV  
 Sbjct: 1656 QVGFSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV  
 1715

Query: 125 QMLSDTLKGLSDRVVFWLWAGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184  
 QML+D L +SD VV FV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW  
 Sbjct: 1716 QMLADNLCNVSDCVVFWTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW  
 1774

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244  
 H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DAIMTRCLA++ F  
 Sbjct: 1775 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAVASVDAIMTRCLAINNAFC  
 1834

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVE 304  
 + V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V  
 Sbjct: 1835 QDVNWDLTYPHIANEDEVNSSCRYLQRMYNACVDALKVNVVYDIGNPKGIKCVRRGDVN  
 1894

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLEFWNCNVDRYPANAIVCRFDTRVLS 364  
 ++FYD P + E Y Y H DKF DG+C+FWNCNVDP YP N++VCR+DTR LS  
 Sbjct: 1895 FRFYDKNPIVRNVKQFE--YDYNQHKDKFADGLCMFWNCNVDCYPDNSLVCRYDTRNLS  
 1951

Query: 365 NLNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHKGQVVSIDIDYVP 424  
 NLPGC+GGSLYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V  
 Sbjct: 1952 VFNLPGCNGGSLYVNKHAFYTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS  
 2010

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484  
 L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ  
 Sbjct: 2011 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ  
 2070

Query: 485 SL 486  
 S+  
 Sbjct: 2071 SI 2072

>gi|133594|sp|P26314|RRPB\_IBVB RNA-DIRECTED RNA POLYMERASE (ORF1B)  
 gi|74826|pir||VFIHB2 genome polyprotein - avian infectious bronchitis  
 virus (strain  
 Beaudette)  
 gi|292953|gb|AAA70234.1| pol protein [Avian infectious bronchitis virus]  
 gi|331173|gb|AAA46224.1| ORF1b [Avian infectious bronchitis virus]  
 Length = 2652

Score = 570 bits (1469), Expect = e-161  
 Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPL 64  
 ++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP  
 Sbjct: 1538 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDEATHACGTNIGTNLPP  
 1597

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIV 124  
 Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV  
 Sbjct: 1598 QVGFSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGQFNHLRVLFKSAKPWHVIRPRIV  
 1657

Query: 125 QMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184  
 QML+D L +SD VVFFV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW

Sbjct: 1658 QMLADNLCNVSDCVVFWTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW  
1716

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244  
H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DAIMTRCLA++ F

Sbjct: 1717 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAVASVDAIMTRCLAINNAFC  
1776

Query: 245 KRVDWSVEYPPIIGDELRVNSACRKYQHMVKSALLADKFPVLHDIGNPKAIKCVPQAEVE 304  
+ V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V

Sbjct: 1777 QDVNWDLTYPHIANEDEVNSSCRYLQRMVNLACVDALKVNVVYDIGNPKGIKCVRRGDVN  
1836

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364  
++FYD P + E Y Y H DKF DG+C+FWNCNVD YP N++VCR+DTR LS

Sbjct: 1837 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNSLVCRYDTRNLS  
1893

Query: 365 NLNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHKGQVVSDDIDYVP 424  
NLPGC+GGSLYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V

Sbjct: 1894 VFNLPGCNGGSLYVNKHAFYTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS  
1952

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484  
L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ

Sbjct: 1953 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ  
2012

Query: 485 SL 486  
S+

Sbjct: 2013 SI 2014

>gi|29293454|gb|AA067706.1| ORF1b polyprotein [Avian infectious bronchitis  
virus]

Length = 2649

Score = 565 bits (1455), Expect = e-160

Identities = 261/482 (54%), Positives = 342/482 (70%), Gaps = 8/482 (1%)

Query: 5 DMTYRRLISMGMFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPL 64  
++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP

Sbjct: 1538 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPP  
1597

Query: 65 QLGSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIV 124  
Q+GFSTG + V P G +DT F VN+K PPG+QF HL L PW+V+R +IV

Sbjct: 1598 QVGFSTGADFVVTPEGLIDTSIGNNFEPVNSKAPPGEQFNHLRALFKSAKPWHVIRPRIV  
1657

Query: 125 QMLSDTLKGLSDRVVFWLWAGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184  
QML+D L +SD VVFW W HG ELT+++YFVKIG E+ C C RAT F++ + YACW

Sbjct: 1658 QMLADNLCNVSDCVVFWTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW  
1716

Query: 185 NHSVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244  
 H +G VYNP ++D+QQWG++GNLQ NHD HC VH+AHVAS DA+MTRCLA++ F  
 Sbjct: 1717 RHCLG---VYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAAHVASADAVMTRCLAINNAFC  
 1773

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVE 304  
 K V+W ++YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V  
 Sbjct: 1774 KDVNWELQYPHIANEDEVNSSCRYLQRMVYNACVDALKVNVVYDIGNPKGIKCVRRGDVN  
 1833

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLEFWNCNVDRYPANAIVCRFDTRVLS 364  
 ++FYD P + E Y Y+ H DKF DG+C+FWNCNVDP YP N++VCR+DTR LS  
 Sbjct: 1834 FRFYDKNPIVPNVKQFE---YDYSQHKDKFADGLCMFWNCNVDCYPENSLVCRYDTRNLS  
 1890

Query: 365 NLNLPGLGCGSLYVKNHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVSDIDYVP 424  
 NLPGC+GGSLYVKNHAFHTP FD+ +F NLK +PFF+Y SPCE+ V+ D V  
 Sbjct: 1891 VFNLPGLGCGSLYVKNHAFHTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS  
 1949

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484  
 L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ F+ YNLW F+ LQ  
 Sbjct: 1950 LATKDCITKCNIGGAVCKKHAQMYAEFVSYNAAVTAGFTFWVTNNFNPNLWKNFSAQ  
 2009

Query: 485 SL 486  
 S+  
 Sbjct: 2010 SI 2011

>gi|25121555|ref|NP\_740631.1| coronavirus nspl1 [Avian infectious  
 bronchitis virus]  
 Length = 521

Score = 559 bits (1440), Expect = e-158  
 Identities = 261/480 (54%), Positives = 342/480 (71%), Gaps = 5/480 (1%)

Query: 5 DMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPL 64  
 ++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP  
 Sbjct: 47 EITYKHLISLLGFKMSVNVGCHNMFITRDEAIRNVRGWGFDVEATHACGTNIGTNLPF 106

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIV 124  
 Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV  
 Sbjct: 107 QVGFSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV 166

Query: 125 QMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184  
 QML+D L +SD VVFV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW  
 Sbjct: 167 QMLADNLCNVSDCVVFTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW 225

Query: 185 NHSVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244  
 H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VH+AHVAS DAIMTRCLA++ F  
 Sbjct: 226 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAAHVASVDAIMTRCLAINNAFC 285

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVE 304  
 + V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V

Sbjct: 286 QDVNWDLTYPHIANEDEVNSSCRYLQRMVNLACVDALKVNVVYDIGNPKGIKCVRRGDVN 345

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364  
 ++FYD P + E Y Y H DKF DG+C+FWNCNVD YP N++VCR+DTR LS

Sbjct: 346 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNSLVCRYDTRNLS 402

Query: 365 NLNLPGLCDGGSGLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVP 424  
 NLPGC+GGSGLYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V

Sbjct: 403 VFNLPGCNGGSGLYVNKHAFYTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS 461

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484  
 L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ

Sbjct: 462 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ 521

>gi|9635157|ref|NP\_058422.1| replicase [Transmissible gastroenteritis virus]

gi|7801348|emb|CAB91143.1| replicase [Transmissible gastroenteritis virus]

Length = 6685

Score = 545 bits (1403), Expect = e-153

Identities = 261/484 (53%), Positives = 335/484 (69%), Gaps = 13/484 (2%)

Query: 4 KDMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLP 63  
 KD+ Y +IS MGF+ + GY +F TR+ A+R+VRAW+GFDVEG H D VGTN+P

Sbjct: 5574 KDVKYANVISYMGFRFEANIPGYHTLFCTRDFAMRNVRAWLGFDVEGAHVCGDNVGTNVP 5633

Query: 64 LQLGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIKI 123  
 LQLGFS GV+ V G V TE V A+ PPG+QF HLIPLM KG PW++VR +I

Sbjct: 5634 LQLGFSNGVDFVVQTEGCVITEKGNSEVVKARAPPGEQFAHLIPLMRKGQPWIVRRRI 5693

Query: 124 VQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIG-PERTCCLCDKRATCFSTSSDTYA 182  
 VQM+ D GLSD ++FVLWA G ELT+M+YFVKIG P++ C C K ATC+S+S YA

Sbjct: 5694 VQMVCDYFDGLSDILIFVLWAGGLELTTRYFVKIGRPQK--CECGKSATCYSSSQSVYA 5751

Query: 183 CWNHSGVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHEC 242  
 C+ H++G DY+YNP+ ID+QQWG+TG+L NH + C +H N HVAS DAIMTRCLA+H+C

Sbjct: 5752 CFKHALGCDYLYNPYCIDIQQWGYTGSLSMNHHEVCNIHRNEHVASGDAIMTRCLAIHDC 5811

Query: 243 FVKRVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAE 302  
 FVKRVDWS+ YP I +E ++N A R VQ V+K+AL +HD+GNPK I+C

Sbjct: 5812 FVKRVDWSIVYPFIDNEEKINKAGRIVQSHVMKAALKIFNPAAIHVDGNPKGIRCA-TTP 5870

Query: 303 VEWKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRV 362  
 + W YD P ++ + L Y Y +H +G+ LFWNCNVD YP +IVCRFDTR

Sbjct: 5871 IPWFCYDRDPINN---NVRCLDYDYMVHGQ--MNGLMLFWNCNVDMYPEFSIVCRFDTRT 5925

Query: 363 LSNLNLPGCDGGSGLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDY 422

S L+L GC+GG+LYVN HAFHTPA+D+ AF LK +PFFYY DS CE V +Y  
 Sbjct: 5926 RSKLSLEGCNGGALYVNNHAFHTPAYDRRAFAKLKPMPPFFYYDDSNCE----LVDGQPNY  
 5981

Query: 423 VPLKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTR 482  
 VPLKS CIT+CN+GGAVC+ HA YR Y++ YN+ + AGF++W + FDTY LW+ F  
 Sbjct: 5982 VPLKSNVCITKCNIGGAVCKKHAALYRAYVEDYNI FMQAGFTIWCPQNFDTYMLWHGFEVN  
 6041

Query: 483 LQSL 486  
 ++L  
 Sbjct: 6042 SKAL 6045

>gi|19387582|ref|NP\_598309.1| Pol1 [porcine epidemic diarrhea virus]  
 gi|13752450|gb|AAK38661.1| Pol1 [porcine epidemic diarrhea virus]  
 Length = 6781

Score = 541 bits (1394), Expect = e-152  
 Identities = 256/480 (53%), Positives = 334/480 (69%), Gaps = 12/480 (2%)

Query: 8 YRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPLQLG 67  
 Y +IS MGF+ + + + +F TR+ A+R+VR W+GFDVEG H VGTN+PLQLG  
 Sbjct: 5675 YEHVISFMGFRFDINIPNHHTLFCTRDFAMRNVRGWLGFDEGAHVVGSNVGTNVPLQLG  
 5734

Query: 68 FSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRKIVQML 127  
 FS GV+ V P G V TE+ V A+ PPG+QF HL+PL+ +G PW+VVR +IVQM  
 Sbjct: 5735 FSNGVDFVVRPEGCVVTESGDYIKPVRARAPPGEQFAHLLPLLKRGQPWDVVRKRIVQMC  
 5794

Query: 128 SDTLKGLSDRVFVLWAGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWNHS 187  
 SD L LSD ++FVLWA G ELT+M+YFVKIGP ++C C K ATC++++ TY C+ H+  
 Sbjct: 5795 SDYLANLSDILIFVLWAGGLELTTMRYFVKIGPSKSCD-CGKVATCYNSALHTYCCFKHA  
 5853

Query: 188 VGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVKRV 247  
 +G DY+YNP+ ID+QQWG+ G+L NH +HC VH N HVAS DAIMTRCLA+H+CFVK V  
 Sbjct: 5854 LGCDYLYNPYCIDIQQWGYKGSLSLNHHEHCNVHRNEHVASGDAIMTRCLAIHDCFVKNV  
 5913

Query: 248 DWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEWKF 307  
 DWS+ YP IG+E +N + R VQ ++S L ++DIGNPK I+C + +W  
 Sbjct: 5914 DWSITYPFIGNEAVINKSGRIVQSHTMRSVLKLYNPKAIYDIGNPKGIRCA-VTDAKWFC  
 5972

Query: 308 YDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSNLN 367  
 +D P + +E Y Y I H +F DG+CLFWNCNVD YP ++VCRFDTR S LN  
 Sbjct: 5973 FDKNPTNSNVKTL-----YDY-ITHGQF-DGLCLFWNCNVDMYPEFSVCRFDTRCRSPLN  
 6027

Query: 368 LPGCDGGSlyVnKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPLKS 427  
 L GC+GGSlyVN HAFHTPAFDK AF LK +PFF+Y D+ C+ ++ I+YVPL++  
 Sbjct: 6028 LEGCNGGSlyVNNHAFHTPAFDKRAFAKLKPMPPFFYYDDTECD----KLQDSINYVPLRA  
 6083



Query: 428 ATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFT-RLQSL 486  
 + CIT+CN+GGAVC H Y Y++AYN SAGF++W+ FDTYNLW TF+ LQ L  
 Sbjct: 6084 SNCITKCNVGGAVCSKHCAMYHSYVNAYNTFTSAGFTIWVPTSFDTYNLWQTFSSNNLQGL  
 6143

>gi|12175747|ref|NP\_073549.1| replicase polyprotein lab [Human coronavirus  
 229E]  
 gi|12082740|gb|AAG48591.1|AF304460\_2 replicase polyprotein lab [Human  
 coronavirus 229E]  
 Length = 6758

Score = 535 bits (1379), Expect = e-151  
 Identities = 254/478 (53%), Positives = 329/478 (68%), Gaps = 13/478 (2%)

Query: 7 TYRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPLQL 66  
 TY +IS MGF+ + + G ++F TR+ A+RHVR W+G DVEG H T D VGTN+PLQ+  
 Sbjct: 5642 TYEHVISYMGFRFDVSMPSGSHSLFCTRDFAMRHVRGWLGMDEGAHVTDGNDVGTNVPLQV  
 5701

Query: 67 GFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRKIVQM 126  
 GFS GV+ VA P G V T + V A+ PPG+QF H++PL+ KG PW+V+R +IVQM  
 Sbjct: 5702 GFSNGVDFVAQPEGCVLTNTGSVVKPVRARAPPGEQFTHIVPLLRKGQPWSVLRRKIVQM  
 5761

Query: 127 LSDTLKGLSDRVVFWLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWNH 186  
 ++D L G SD +VFVLWA G ELT+M+YFVKIG + C C ATC+++ S+ Y C+ H  
 Sbjct: 5762 IADFLAGSSDVLVFWLWAGGLELTMMRYFVKIGAVKH-CQCGTVATCYNVSNDYCCFKH  
 5820

Query: 187 SVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVKR 246  
 ++G DYVYNP++ID+QQWG+ G+L +NH C VH N HVAS DAIMTRCLAV++CFVK  
 Sbjct: 5821 ALGCDYVYNPYVIDIQQWGYVGSLSNHHAI CNVHRNEHVASGDAIMTRCLAVYDCFVK  
 5880

Query: 247 VDWSVEYPIIGDELRVNSACRKYQHMVKSALLADKFPVLHDIGNPKAIKCPQAEVEWK 306  
 VDWS+ YP+I +E +N R VQ ++++A+ +HDIGNPK I+C + +W  
 Sbjct: 5881 VDWSITYPMIANENAINKGGRTVQSHIMRAAIKLYNPKAIHDIGNPKGIRCA-VTDAKWY  
 5939

Query: 307 FYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLEFWNCNVDRYPANAIVCRFDTRVLSNL 366  
 YD P + +E Y Y H DG+CLEFWNCNVDP +IVCRFDTR S L  
 Sbjct: 5940 CYDKNPINSNVKTL---YDYMTHGQ--MDGLCLEFWNCNVDMYPEFSIVCRFDTRTRSTL  
 5994

Query: 367 NLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSID-IDYVPL 425  
 NL G +GGSLYVN HAFHTPA+DK A LK PFFYY D CE VV D ++YVPL  
 Sbjct: 5995 NLEGVNGGSLYVNNHAFHTPAYDKRAMAKLPAPFFYYDDGSCE-----VVHDQVNYVPL  
 6049

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRL 483  
 ++ CIT+CN+GGAVC HAN YR Y+++YN+ AGF++W+ FD YNLW TFT +  
 Sbjct: 6050 RATNCITKCNIGGAVCSKHANLYRAYVESYNIFTQAGFNIWVPTTFDCYNLWQTFTEV 6107

>gi|133591|sp|P18458|RRPB\_BEV RNA-directed RNA polymerase (ORF1B)  
 gi|94017|pir||S11238 polymerase - Berne virus  
 gi|1334814|emb|CAA36601.1| 2nd polymerase reading frame (AA 1-2291)  
 [Berne virus]

Length = 2291

Score = 50.1 bits (118), Expect = 8e-05

Identities = 37/103 (35%), Positives = 54/103 (52%), Gaps = 11/103 (10%)

Query: 140 FVLWAHGFELTSMKYFVKIGPERTC--CLCDKRATCFSTSSDTYACWNHSGVF--DYVYN 195  
 F+L++ +L S+K++V+ TC C C + A C + Y C N G + N  
 Sbjct: 1511 FILYSCSNDLKSLKFYVEFD---TCYFCSCGEMAICLMRDGN-YKCRNCYGGMLISKLVN  
 1566

Query: 196 PFMIDVQQWGFTGNLQSNHDQHC-QVHGNAHVASCDAIMTRCL 237

+DVQ+ LQ HD C Q HG++H A CDA+MT+CL

Sbjct: 1567 CKYLDVQKERV--KLQDAHDAICQQFHGDSHEALCDAVMTKCL 1607

>gi|1513061|dbj|BAA13323.1| cyanoprotein alpha subunit precursor  
 [Riptortus clavatus]

Length = 693

Score = 34.7 bits (78), Expect = 3.7

Identities = 16/36 (44%), Positives = 22/36 (61%), Gaps = 1/36 (2%)

Query: 371 CDGGS LYVNKHAFTPAFDKSAFTNLKQLPFFYYSD 406

C G LY +KHA P FD+ A+ + Q+P FY+ D

Sbjct: 643 CGGSKLYDSKHAMGFP-FDRPAYPDAFQVPNFYFKD 677

Database: All non-redundant GenBank CDS  
 translations+PDB+SwissProt+PIR+PRF

Posted date: Apr 11, 2003 2:30 AM

Number of letters in database: 454,141,287

Number of sequences in database: 1,411,415

Lambda	K	H
0.325	0.139	0.456

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 473,361,261

Number of Sequences: 1411415

Number of extensions: 20503315

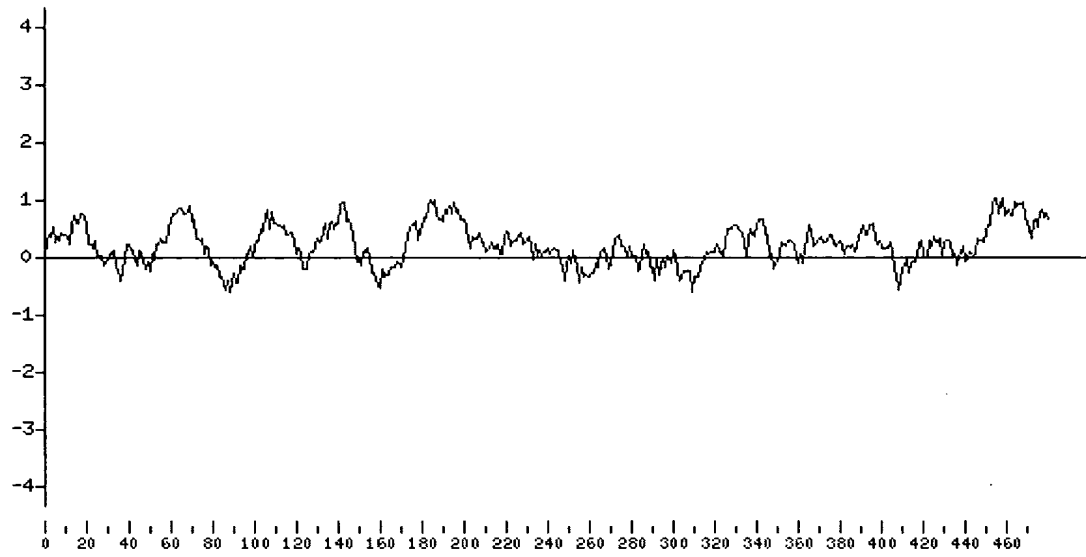
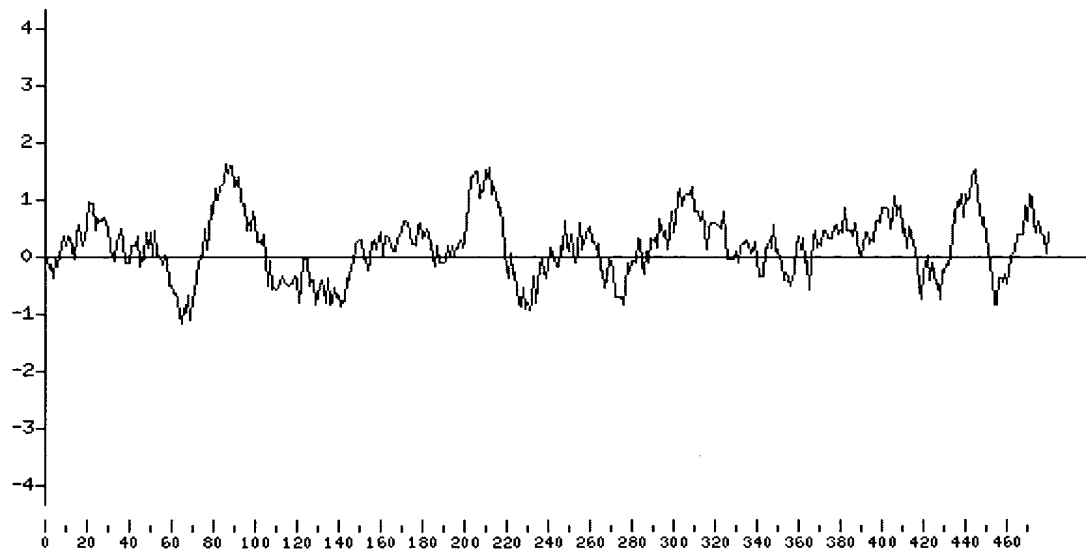
Number of successful extensions: 51018

Number of sequences better than 10.0: 27

Number of HSP's better than 10.0 without gapping: 26

Number of HSP's successfully gapped in prelim test: 1

Number of HSP's that attempted gapping in prelim test: 50937  
Number of HSP's gapped (non-prelim): 33  
length of query: 486  
length of database: 454,141,287  
effective HSP length: 127  
effective length of query: 359  
effective length of database: 274,891,582  
effective search space: 98686077938  
effective search space used: 98686077938  
T: 11  
A: 40  
X1: 15 ( 7.0 bits)  
X2: 38 (14.6 bits)  
X3: 64 (24.7 bits)  
S1: 40 (21.6 bits)  
S2: 75 (33.5 bits)

**FIGURE 125****FIGURE 125A****FIGURE 125B**

**FIGURE 126****5'3' Frame 1**

QVHQNVCVL-LIFYLMTLSR--SHKICQ-FQKWSRLQLTMLKFHSCFGVRMDMLKPSTQN  
YKQVKRGNQVLRCLTCTRCKEFLKSVTFRIMVKMLLYQKE---MSQSILNCVNT-IHLL  
-LYPPT-ELFTLVL

**5'3' Frame 2**

RFIKMCVFCD-SFT--LCRDNKVTRFVSDFKSGQGYN-LC-NFIHALV-GWTC-NLLPKT  
TSKSSVATRCCDA-LVQDAKNAS-KV-PSELW-KCCYTKRNNDECRKVYSTVSILKYTYF  
SCTLQHESYSLWCW

**5'3' Frame 3**

GSSKCVCSVIDLLLDDEVEIIKSQDLSVISKVVKVTIDYAEISFMLWCKDGHVETFYPKL  
QASQAWQPGVAMPNLYKMQRMLLEKCDLQNYGENAVIPKGIMMNVAKYTQLCQYLNTLTL  
AVPSNMRVIHFGAG

**3'5' Frame 1**

PAPK-ITLMLEGTAKVSVFKY-HS-VYFATFIIIPFGITAFSP-F-RSHFSRSILCILYK  
LGIATPGCHA-LACSGF-KVSTCPSLHQSMNEISA-SIVTLTTFEITDKSCDFIISTKSS  
SKRSITEHTHFDEP

**3'5' Frame 2**

QHQSE-LSCWRVQLK-VYLSIDTVEYTLRHSSLFLLV-QHFHHNSEGHTFQEAFASCTS  
-ASQHLVATLDLLVVLGRRFQHVHPYTKA-MKFQHSQ-L-P-PLLKSLTNLVTLISRQSHQ  
VKDQSQNTHILMNL

**3'5' Frame 3**

STKVNNSHVGGYS-SKCI-VLTQLSILCDIHHYSFWYNSIFTIILKVTLFKKHSLSHLVQV  
RHRNTWLPRLTCL-FWVEGFNMSILTPKHE-NFSIVNCNLDHF-NH-QIL-LYYLDKVIK  
-KINHRHTHF-T

**FIGURE 127****5'3' Frame 1**

-VFTYPGKANQPRSLVDLFSKRTN-NV--WTPIKPT-CPPHYIWWTHRFN-Q-PEWRTAM  
GQGQNSADPKVYPIILRLGSQLSLSMARRNLDSEARAFQSTPIVVQMTKLATTEELPDE  
FVVVTAK-KSSAPDGTSIT-ELAQKLHFPTALTKKASYGLQLREP-IHPKTTLAPAILIT  
MLPPCYNFLKEQHCQKASTQREAEAAVKPLLAPHHVVAVIQEIQLLA AVGEILLLEWLAE  
VVKLPSRYCC-TD-TSLRAKFLVKANNKAKLSLRNLLLRHLKSLAKNVLPQNSTTSLKH  
LGDVVQNKPKEISGTKT-SDKELITNIGPQIAQFA

**5'3' Frame 2**

RFLPTQEKPNTDLL-ICSLNEQIKMSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGLQW  
GKAKTAPTFRFTQ-YCVLVHSSSAWQGGT-IPSRPGRSNQHQ-WSR-PNWLLPKSYPTS  
SWW-RQNERAQPMVLLLPRNWPRSFTSLRR-QRRHRMGCN-GSLEYTORPHWHPQS--Q  
CCHRATTSSRNIAKRLLRGKQRRQSSLESLLIT-SR-FKKFNSWQQ-GKFSCSNG-RR  
W-NCPRAIARQIEPA-EQSFW-RPTTTRPNCH-EICC-GI-KASPKTYCHKTVQRHSSI  
WETWSRTNPRKFRGPRPNQTRN-LQTLGRKLHNL

**5'3' Frame 3**

GFYLPKRSQPTSISCRSVL-TNKLKCLIMDPNQTNVVPALHLVDPQIQLTITRMEDCNG  
ARPKQRRPQGLPNNIASWFTALTQHGKEELRFPRGQGVPIINTNSGPDDQIGYYRRATRRV  
RGGDGKMKELSPRWYFYLLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNN  
AATVLQLPQGTTLPKGFYAEGSRGGSQASSRSSRSRGNSTPGSSRGNSPARMASGG  
GETALALLLLDRLNQLESKVSGKGQQQQGQTVTKKSAAEASKKPRQKRTATKQYNVTQAF  
GRRGPEQTQGNFGDQDLIRQGTQDYKHWAACTIC

**3'5' Frame 1**

RQIVQFAAQCL-SVPCLIRSWSPKFPWVCSGPRLPNA-VTLYCFVAVRFWRGFLDASAAD  
FLVTVPCCCWPLPETLLSSWFNLSSSNSARAVSPPPLAIRAGEFPLLLPGVEFLELPRL  
RDEEREEA-LPPLLPSA-KPFGNVVP-GSCSTVAALLGLRVPMWSLGVFKAPSVATHM  
PSLLAP-GSEASGPVPR--KYHLGLSSFILPSPRTRRVALR--PIWSSGPLLVLIGTPW  
PRGNLSSSLPC-VRAVNQDAILLGKPWGRRCFGLAPLQSSILVIVS-ICGSTKCNAGGTT  
LV-LGSIIRHFNLFV-RTDLQEIEVGWLFGLGR-KP

**3'5' Frame 2**

GKLCNLRPNVCNQFLV-LGLGPRNFLGFVLDHVSQMLE-RCTVLWQYVFGEAF-MPQQQI

S--QFGLVVVGLYQKLCSQAGSICLAAIARGQFHHLR-PFEQENFPYCCQELNFLNYRDY  
 VMRSEKRLDCRLCFPLRRSLLAMLFLEEVVARWQHGY-DCGCQCGLWVYSRLPQLQPIRC  
 LLC-RRREVKLLGQFLGNRSTIWG-ALSFCRHHHELVG-LFGSSQFGHLDHYWC-LERPG  
 LEGI-VPPCHAE-EL-TKTQYYWVNLGVGAVLALPHCSPPFWLLSVESVGPPNVMRGALR  
 WFDWGPLSDILICSFREQIYKRSRLVGFSWVGKNL

### 3'5' Frame 3

ANCAICGPMFVISSLSLSD-VLVPEISLGLFWTTSPKCLSDVVLFCGSTFLARLFRCLSSRF  
 LSDSLALLLLAFTRNFAKLQSV-QQ-REGSFTTSASHSSRRISPTAARS-IS-ITATT  
 --GARRGLTAASASLCVEAFWQCCSLRKL-HGGSIVIRIAGANVVFVGC IQGSLSCNPYDA  
 FFVSAVGK-SFWASS-VIEVPSGAELFHFAVTTTNSGSSSVVANLVIWTTIGVDWNALA  
 SRESKFLAMLSESCPEPRNIIG-TLGSALFWPCPIAVLHSGYCQLNLWVHQM-CGGHYV  
 GLIGVHYQTF-FVRLNRSTRDRGWLAFFPG-VKT

### FIGURE 128

-GLELKL-LTSICAF-PFCYSLF--CLLYFGFHKSRI-KNLVPKSKRT-NFSLF-LVFL  
 YAVAYAL-YSAVHLINLMCLKILVRYNTRGNTYSTAWLCALGKVLPHRWHTMVQTCTPN  
 VTINCQDPAGGALIARCWYLHEGHQTAAFRDVLVVLNKRNT-NV--WTPIKPT-CPPHYI  
 WWTHRFN-Q-PEWRTQWGKAKTAPTPTFTQ-YCVLVHSSHSAWQGGT-IPSRPGRSNQHQ  
 -WSR-PNWLLPKSYPTSSWW-RQNERAQPMVLLLPRNWPRSFTSLRR-QRRHRMGCN-G  
 SLEYTQRPWHHPQS--QCCHRATTSSRNNAKRLLRGKQRRQSSLSLLIT-SR-FKKF  
 NSWQQ-GKFSCSNG-RRW-NCPRAIARQIEPA-EQSFV-RPTTTRPNCH-EICC-GI-K  
 ASPKTYCHKTQVRHSSIWETWSRTNPRKFRGPRPNQTRN-LQTLAANCTICKKCLCILWN  
 VTHWHGSHTFGNMADLSWSH-IG-QRSTIQQRHTAEQAH-RIQNIPTNRA-KGQKEKD-  
 -SSAFAAETKEAAHCDSSSC

EDSSSSFN-LLFVLFSLSAIPCFNNAYYILVFTRNPGSRRTLYQSLNEHETSHCFDLYFS  
 MQLHMHCTALCI--TSCA-RSL-GTTLGVLIALLLGFVL-ERFYLFIDGTLWFKHAHLM  
 LLSTVKIQLVVRL-LGVGTFMKVTKLLHLETYLLF-INEQIKMSDNGPQSNQRSAPRITF  
 GGPTDSTDNNQNGGRNGARPKQRRPQGLPNNIASWFTALTQHGKEELRFPRGQGVPIINTN  
 SGPDDQIGYYRRATRRVRGGDGKMKELSPRWYFYLLGTGPEASLPYGANKEGIVWVATEG  
 ALNTPKDHIGTRNPNNNAATVLQLPQGTTLPGFYAEGSRGGSQASSRSSRSRGNNSRNS  
 TPGSSRGNSPARMASGGGETALALLLLDRLNQLESKVSQGGQGGQTVTKKSAAEASKK  
 PRQKRTATKQYNVTQAFGRGPEQTQGNFGDQDLIRQGTQDYKHWPQIAQFAPSASAFFGM  
 SRIGMEVTPSGTWLTYHGAIKLDDKDPQFKDNVILLNKHIDAYKTFPPTPKDKKKKTD  
 EAQPLPQRQKKQPTVTLLP

RTRAQALIDFYLCFLAFLFLVLIMLIIFWFSLEIQDLEEPCTKV-TNMKLLIVLTCISL  
 CSCICTVQRCASNKPHVLEDPCVKQH-G-YL-HCLALCSRKGFTFS-MAHYGSNMHT-C  
 YYQLSRSSWWCAYS-VLVPS-RSPNCCI-RRTCCFK-TNKLKCLIMDPNQTNVVPALHL  
 VDPQIQLTITRMEDAMGQGQNSADPKVYPIILRLGSQSLSMARRNLDSEARAFQSTPI  
 VVQMTKLATTEELPDEFVVVTAK-KSSAPDGTSIT-ELAQKLHFPTALTKKASYGLQRE  
 P-IHPKTTLAPAILITMLPPCYNFLKEQHCQKASTQREAEAAVKPLLAPHHVVAVIQEIQ  
 LLAAVGEILLLEWLAEVVKLPSRYCC-TD-TSLRAKFLVKANNKAKLSLRNLLLRHLKS  
 LAKNVLPQNSTTSLKHLGDVVQNKPKKEISGTKT-SDKELITNIGRKLHNLLQVPLHSLEC  
 HALAWKSHLREHG-LIMEPLNWMTKIHNSKTTSYC-TSTLTHTKHSQQSLKRTKRKRLM  
 KLSLCRRDKRSSPL-LFFL

### FIGURE 129

#### 5'3' Frame 1

taccgtagactcatctctatgatgggtttcaaaatgaattaccaagtcaatgggttacct  
 Y R R L I S M M G F K M N Y Q V N G Y P  
 aatatgtttatcacccgcgaagaagctattcgtcacgttcgtgcgtggattggctttgat  
 N M F I T R E E A I R H V R A W I G F D  
 gtagagggctgtcatgcaactagagatgctgtgggtactaacctacctctccagctagga  
 V E G C H A T R D A V G T N L P L Q L G  
 ttttctacaggtgttaacttagtagctgtaccgactgggttatgttgacactgaaaataac  
 F S T G V N L V A V P T G Y V D T E N N  
 acagaattcaccagagttaatgcaaaacctccaccaggtgaccagtttaaacatcttatacc  
 T E F T R V N A K P P P G D Q F K H L I

#### 5'3' Frame 2

taccgtagactcatctctatgatgggtttcaaaatgaattaccaagtcaatgggttaccta  
 T V D S S L - W V S K - I T K S M V T L  
 atatgtttatcacccgcgaagaagctattcgtcacgttcgtgcgtggattggctttgatg  
 I C L S P A K K L F V T F V R G L A L M  
 tagagggctgtcatgcaactagagatgctgtgggtactaacctacctctccagctaggat  
 - R A V M Q L E M L W V L T Y L S S - D  
 ttttctacaggtgttaacttagtagctgtaccgactgggttatgttgacactgaaaataaca  
 F L Q V L T - - L Y R L V M L T L K I T  
 cagaattcaccagagttaatgcaaaacctccaccaggtgaccagtttaaacatcttatacc  
 Q N S P E L M Q N L H Q V T S L N I L Y



**5'3' Frame 3**

taccgtagactcatctctatgatgggtttcaaaatgaattaccaagtcaatgggttaccctaa  
P - T H L Y D G F Q N E L P S Q W L P -  
tatgtttatcacccgcgaagaagctattcgtcacgttcgtgctggattggctttgatgt  
Y V Y H P R R S Y S S R S C V D W L - C  
agagggctgtcatgcaactagagatgctgtgggtactaacctacctctccagctaggatt  
R G L S C N - R C C G Y - P T S P A R I  
ttctacaggtgttaacttagtagctgtaccgactgggttatgttgacactgaaaataacac  
F Y R C - L S S C T D W L C - H - K - H  
agaattcaccagagttaatgcaaaacctccaccaggtgaccagtttaaacatcttataacc  
R I H Q S - C K T S T R - P V - T S Y T

**3'5' Frame 1**

ggtataagatgtttaaactggtcacctgggtggaggttttgcattaactctggtgaattct  
G I R C L N W S P G G G F A L T L V N S  
gtgttattttcagtggtcaacataaccagtcggtacagctactaagttaacacctgtagaa  
V L F S V S T - P V G T A T K L T P V E  
aatcctagctggagaggttaggttagtaccacagcatctctagttgcatgacagccctct  
N P S W R G R L V P T A S L V A - Q P S  
acatcaaagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacata  
T S K P I H A R T - R I A S S R V I N I  
ttagggtaaccattgacttggtaattcattttgaaacccatcatagagatgagtctacggta  
L G - P L T W - F I L K P I I E M S L R

**3'5' Frame 2**

ggtataagatgtttaaactggtcacctgggtggaggttttgcattaactctggtgaattctg  
V - D V - T G H L V E V L H - L W - I L  
tggtattttcagtggtcaacataaccagtcggtacagctactaagttaacacctgtagaaa  
C Y F Q C Q H N Q S V Q L L S - H L - K  
atcctagctggagaggttaggttagtaccacagcatctctagttgcatgacagccctcta  
I L A G E V G - Y P Q H L - L H D S P L  
catcaaagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatat  
H Q S Q S T H E R D E - L L R G - - T Y  
tagggtaaccattgacttggtaattcattttgaaacccatcatagagatgagtctacggta  
- G N H - L G N S F - N P S - R - V Y G

**3'5' Frame 3**

ggtataagatgttttaaactgggtcacctgggtggaggttttgcattaactctggtgaattctgt  
 Y K M F K L V T W W R F C I N S G E F C  
 gttattttcagtggtcaacataaccagtcggtacagctactaagttaacacctgtagaaaa  
 V I F S V N I T S R Y S Y - V N T C R K  
 tcctagctggagaggttaggttagtacccacagcatctctagttgcatgacagccctctac  
 S - L E R - V S T H S I S S C M T A L Y  
 atcaaagccaatccacgcacgaacgtgacgaatagcttcttcgcggtgataaacatatt  
 I K A N P R T N V T N S F F A G D K H I  
 agggtaaccattgacttggttaattcattttgaaacccatcatagagatgagtctacggta  
 R V T I D L V I H F E T H H R D E S T V

**FIGURE 130**

	10	20	30	40	50	60
SEQ ID NO: 9997	KGHDLRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLP					
SEQ ID NO:10034	----YRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLP					
	*****					
Prim. Cons.	KGHD2RRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLP					

	70	80	90	100	110	120
SEQ ID NO: 9997	LQLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLMYKGLPWNVVRKI					
SEQ ID NO:10034	LQLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLI-----					
	*****:*****:.....:*****					
Prim. cons.	LQLGFSTGVNLVAVPTGYVDTENNT2FTRVNA22222QFKHLIPLMYKGLPWNVVRKI					

	130	140	150	160	170	180
SEQ ID NO: 9997	VQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYAC					
SEQ ID NO:10034	-----					

Prim. cons.	VQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYAC					
-------------	---	--	--	--	--	--

	190	200
SEQ ID NO: 9997	WNHSVGFQDYVYNPFMIDVQQWGLYG	
SEQ ID NO:10034	-----	

**FIGURE 131****5'3' Frame 1**

caggttcatcaaaaatgtgtgtgttctgtgattgatcttttacttgatgactttgtcgaga  
 Q V H Q N V C V L - L I F Y L M T L S R  
 taataaagtcacaagatttgtcagtgatttcaaaagtgggtcaagggttacaattgactatg  
 - - S H K I C Q - F Q K W S R L Q L T M  
 ctgaaatttcattcatgctttgggtgtaaggatggacatggtgaaaccttctacccaaaac  
 L K F H S C F G V R M D M L K P S T Q N  
 tacaagcaagtcaagcgtggcaaccaggtggtgcatgcctaacttgataagatgcaaa  
 Y K Q V K R G N Q V L R C L T C T R C K  
 gaatgcttcttgaaaagtgtgaccttcagaattatgggtgaaaatgctgttatacaaaag  
 E C F L K S V T F R I M V K M L L Y Q K  
 gaataatgatgaatgtcgcaaagtataactcaactgtgtcaataacttaatacacttactt  
 E - - - M S Q S I L N C V N T - I H L L  
 tagctgtaccctccaacatgagagttattcactttgggtgctgg  
 - L Y P P T - E L F T L V L

**5'3' Frame 2**

caggttcatcaaaaatgtgtgtgttctgtgattgatcttttacttgatgactttgtcgagat  
 R F I K M C V F C D - S F T - - L C R D  
 aataaagtcacaagatttgtcagtgatttcaaaagtgggtcaagggttacaattgactatgc  
 N K V T R F V S D F K S G Q G Y N - L C  
 tgaaatttcattcatgctttgggtgtaaggatggacatggtgaaaccttctacccaaaact  
 - N F I H A L V - G W T C - N L L P K T  
 acaagcaagtcaagcgtggcaaccaggtggtgcatgcctaacttgataagatgcaaa  
 T S K S S V A T R C C D A - L V Q D A K  
 aatgcttcttgaaaagtgtgaccttcagaattatgggtgaaaatgctgttatacaaaagg  
 N A S - K V - P S E L W - K C C Y T K R  
 aataatgatgaatgtcgcaaagtataactcaactgtgtcaataacttaatacacttacttt  
 N N D E C R K V Y S T V S I L K Y T Y F  
 agctgtaccctccaacatgagagttattcactttgggtgctgg  
 S C T L Q H E S Y S L W C W

**5'3' Frame 3**

caggttcatcaaaaatgtgtgtgttctgtgattgatcttttacttgatgactttgtcgagata  
 G S S K C V C S V I D L L L D D F V E I  
 ataaagtcacaagatttgtcagtgatttcaaaagtgggtcaagggttacaattgactatgct  
 I K S Q D L S V I S K V V K V T I D Y A  
 gaaatttcattcatgctttgggtgtaaggatggacatggtgaaaccttctacccaaaacta  
 E I S F M L W C K D G H V E T F Y P K L  
 caagcaagtcaagcgtggcaaccaggtggtgcatgcctaacttgataagatgcaaa  
 Q A S Q A W Q P G V A M P N L Y K M Q R

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atgcttcttgaaaagtgtgaccttcagaattatgggtgaaaatgctgttataccaaaaagga  
 M L L E K C D L Q N Y G E N A V I P K G  
 ataatgatgaatgtcgcgcaaagtataactcaactgtgtcaataacttaaatacacttacttta  
 I M M N V A K Y T Q L C Q Y L N T L T L  
 gctgtaccctccaacatgagagttattcacttttggtgctgg  
 A V P S N M R V I H F G A

**3'5' Frame 1**

ccagcaccaaagtgaataactctcatgttggagggtacagctaaagtaagtgtattttaag  
 P A P K - I T L M L E G T A K V S V F K  
 tattgacacagttgagtatactttgcgacattcatcattattccttttggtataacagca  
 Y - H S - V Y F A T F I I I P F G I T A  
 ttttcaccataattctgaaggtcacacttttcaagaagcattcctttgcatcttgtacaag  
 F S P - F - R S H F S R S I L C I L Y K  
 ttaggcacgcgaacacctgggtgccacgcttgacttgctttagttttgggtagaagggtt  
 L G I A T P G C H A - L A C S F G - K V  
 tcaacatgtccatccttacaccaaagcatgaatgaaatttcagcatagtcaattgtaacc  
 S T C P S L H Q S M N E I S A - S I V T  
 ttgaccacttttgaaatcactgacaaatcttgtgactttattatctcgacaaagtcacaa  
 L T T F E I T D K S C D F I I S T K S S  
 agtaaaagatcaatcacagaacacacacattttgatgaacctg  
 S K R S I T E H T H F D E P

**3'5' Frame 2**

ccagcaccaaagtgaataactctcatgttggagggtacagctaaagtaagtgtattttaagt  
 Q H Q S E - L S C W R V Q L K - V Y L S  
 attgacacagttgagtatactttgcgacattcatcattattccttttggtataacagcat  
 I D T V E Y T L R H S S L F L L V - Q H  
 ttttcaccataattctgaaggtcacacttttcaagaagcattcctttgcatcttgtacaagt  
 F H H N S E G H T F Q E A F F A S C T S  
 taggcacgcgaacacctgggtgccacgcttgacttgctttagttttgggtagaagggtt  
 - A S Q H L V A T L D L L V V L G R R F  
 caacatgtccatccttacaccaaagcatgaatgaaatttcagcatagtcaattgtaacct  
 Q H V H P Y T K A - M K F Q H S Q L - P  
 tgaccacttttgaaatcactgacaaatcttgtgactttattatctcgacaaagtcacaa  
 - P L L K S L T N L V T L L S R Q S H Q  
 gtaaaagatcaatcacagaacacacacattttgatgaacctg  
 V K D Q S Q N T H I L M N L

**3'5' Frame 3**

ccagcaccaaagtgaataactctcatgttggagggtacagctaaagtaagtgtattttaagta  
 S T K V N N S H V G G Y S - S K C I - V

ttgacacagttgagtatactttgcgacattcatcattattccttttgggtataacagcatt  
 L T Q L S I L C D I H H Y S F W Y N S I  
 ttcaccataattctgaaggtcacacttttcaagaagcattctttgcatcttgtacaagtt  
 F T I I L K V T L F K K H S L H L V Q V  
 aggcacgcgaacacctgggtgccacgcttgacttgctttagttagtttgggtagaaggtttc  
 R H R N T W L P R L T C L - F W V E G F  
 aacatgtccatccttacaccaagcatgaatgaaatttcagcatagtcaattgtaacctt  
 N M S I L T P K H E - N F S I V N C N L  
 gaccacttttgaaatcactgacaaatcttgtgactttattatctcgacaaagtcataag  
 D H F - N H - Q I L - L Y Y L D K V I K  
 taaaagatcaatcacagaacacacacattttgatgaacctg  
 - K I N H R T H T F - - T

### FIGURE 132

#### 5'3' Frame 1

taggtttttacctaaccaggaagccaaacacctcgatctctttagatctgttctct  
 - V F T Y P G K A N Q P R S L V D L F S  
 aaacgaacaaattaaaatgtctgataatggacccaatcaaaccaacgtagtgcccccg  
 K R T N - N V - - W T P I K P T - C P P  
 cattacatttgggtggaccacagattcaactgacaataaccagaatggaggactgcaatg  
 H Y I W W T H R F N - Q - P E W R T A M  
 gggcaaggccaaaacagcgccgacccaaggtttacccaataatattgcttcttgggttca  
 G Q G Q N S A D P K V Y P I I L R L G S  
 cagctctcactcagcatggcaaggaggaacttagattccctcgaggccaggcggttccaa  
 Q L S L S M A R R N L D S L E A R A F Q  
 tcaacaccaatagtggtccagatgaccaaattggctactaccgaagagctacccgacgag  
 S T P I V V Q M T K L A T T E E L P D E  
 ttcgtgggtggtagcgcaaaatgaaagagctcagccccagatggtagtcttattacctag  
 F V V V T A K - K S S A P D G T S I T -  
 gaactggcccagaagcttcacttccctacggcgctaacaaagaaggcatcgtaggggttg  
 E L A Q K L H F P T A L T K K A S Y G L  
 caactgagggagccttgaatacacccaaagaccacattggcacccgcaatcctaataaca  
 Q L R E P - I H P K T T L A P A I L I T  
 atgctgccaccgtgctacaacttccctcaaggaacaacattgccaaaaggcttctacgcag  
 M L P P C Y N F L K E Q H C Q K A S T Q  
 agggaagcagaggcggcagtcagcctcttctcgctcctcatcacgtagtcgcggttaatt  
 R E A E A A V K P L L A P H H V V A V I  
 caagaaattcaactcctggcagcagtaggggaaattctcctgctcgaatggctagcggag  
 Q E I Q L L A A V G E I L L L E W L A E  
 gtgggtgaaactgccctcgcgctattgctgctagacagattgaaccagcttgagagcaaag  
 V V K L P S R Y C C - T D - T S L R A K  
 tttctggtaaaggccaacaacaagaaggccaaactgtcactaagaaatctgctgctgagg

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F L V K A N N N K A K L S L R N L L L R  
catctaaaaagcctcgccaaaaacgtactgccacaaaacagtacaacgtcactcaagcat  
H L K S L A K N V L P Q N S T T S L K H  
ttgggagacgtggtccagaacaaacccaaggaaatttcggggaccaagacctaatacagac  
L G D V V Q N K P K E I S G T K T - S D  
aaggaaactgattacaaacattggggccgcaaattgcacaatttgcct  
K E L I T N I G P Q I A Q F A

**5'3' Frame 2**

taggtttttacctaccaggaagccaaacacctcgatctctttagatctgttctcta  
R F L P T Q E K P T N L D L L - I C S L  
aacgaacaaattaaaatgtctgataatggacccaatcaaaccaacgtagtgtccccgc  
N E Q I K M S D N G P Q S N Q R S A P R  
attacatttgggtggaccacagattcaactgacaataaccagaatggaggactgcaatgg  
I T F G G P T D S T D N N Q N G G L Q W  
ggcaaggccaaaaacagcgccgacccaagggtttaccaataatattgcgtcttgggtcac  
G K A K T A P T P R F T Q - Y C V L V H  
agctctcactcagcatggcaaggaggaacttagattccctcgaggccagggcggttccaat  
S S H S A W Q G G T - I P S R P G R S N  
caacaccaatagtgggtccagatgaccaaattgggtactaccgaagagctacccgacgagt  
Q H Q - W S R - P N W L L P K S Y P T S  
tcgtgggtgggtgacggcaaaatgaaagagctcagccccagatggtacttctattacctagg  
S W W - R Q N E R A Q P Q M V L L L P R  
aactggcccagaagcttcacttccctacggcgctaacaagaaggcatcgtagtgggttgc  
N W P R S F T S L R R - Q R R H R M G C  
aactgagggagccttgaatacacccaaagaccacattggcaccgcaatcctaataacaa  
N - G S L E Y T Q R P H W H P Q S - - Q  
tgctgccaccgtgctacaacttccctcaaggaacaacattgccaaaaggcttctacgcaga  
C C H R A T T S S R N N I A K R L L R R  
gggaagcagagggcggcagtcaggcctcttctcgctcctcatcacgtagtcgcggtaatc  
G K Q R R Q S S L F S L L I T - S R - F  
aagaaattcaactcctggcagcagtaggggaaattctcctgctcgaatggctagcggagg  
K K F N S W Q Q - G K F S C S N G - R R  
tggtgaaactgccctcgcgctattgctgctagacagattgaaccagcttgagagcaaagt  
W - N C P R A I A A R Q I E P A - E Q S  
ttctggtaaaaggccaacaacaagaaggccaaactgtcactaagaaatctgctgctgaggc  
F W - R P T T T R P N C H - E I C C - G  
atctaaaaagcctcgccaaaaacgtactgccacaaaacagtacaacgtcactcaagcatt  
I - K A S P K T Y C H K T V Q R H S S I  
tgggagacgtggtccagaacaaacccaaggaaatttcggggaccaagacctaatacagaca  
W E T W S R T N P R K F R G P R P N Q T  
aggaactgattacaaacattggggccgcaaattgcacaatttgcct  
R N - L Q T L G R K L H N L P

**5'3' Frame 3**

taggtttttacctacccaggaaaagccaaccaacctcgatctctttagtagatctgttctctaa  
 G F Y L P R K S Q P T S I S C R S V L -  
 acgaacaaattaaaaatgtctgataatggaccccaatcaaaccaacgtagtgcccccgca  
 T N K L K C L I M D P N Q T N V V P P A  
 ttacatttggtggacccacagattcaactgacaataaccagaatggaggactgcaatggg  
 L H L V D P Q I Q L T I T R M E D C N G  
 gcaaggccaaaacagcgccgaccccaaggtttacccaataatattgcgtcttggttcaca  
 A R P K Q R R P Q G L P N N I A S W F T  
 gctctcactcagcatggcaaggaggaacttagattccctcgaggccaggcggttccaatc  
 A L T Q H G K E E L R F P R G Q G V P I  
 aacaccaatagtggtccagatgaccaaattggctactaccgaagagctacccgacgagtt  
 N T N S G P D D Q I G Y Y R R A T R R V  
 cgtggtggtgacggcaaaatgaaagagctcagccccagatgggtacttctattacctagga  
 R G G D G K M K E L S P R W Y F Y Y L G  
 actggcccagaagcttcacttccctacggcgctaacaagaaggcatcgtagtgggttgca  
 T G P E A S L P Y G A N K E G I V W V A  
 actgagggagccttgaatacacccaaagaccacattggcaccgcgaatcctaataacaat  
 T E G A L N T P K D H I G T R N P N N N  
 gctgccaccgtgctacaacttccctcaaggaacaacattgccaaaaggcttctacgcagag  
 A A T V L Q L P Q G T T L P K G F Y A E  
 ggaagcagaggcggcagtcagcctcttctcgctcctcatcacgtagtcgcggttaattca  
 G S R G G S Q A S S R S S S R S R G N S  
 agaaattcaactcctggcagcagtaggggaaatttctcctgctcgaatggctagcggaggt  
 R N S T P G S S R G N S P A R M A S G G  
 ggtgaaactgccctcgcgctattgctgctagacagattgaaccagcttgagagcaaagtt  
 G E T A L A L L L L D R L N Q L E S K V  
 tctggtaaaggccaacaacaagaaggccaaactgtcactaagaaatctgctgctgaggga  
 S G K G Q Q Q Q G Q T V T K K S A A E A  
 tctaaaaagcctcgccaaaaacgtactgccacaaaacagtacaacgtcactcaagcattt  
 S K K P R Q K R T A T K Q Y N V T Q A F  
 gggagacgtggtccagaacaaacccaaggaaatttcggggaccaagacctaatacagacaa  
 G R R G P E Q T Q G N F G D Q D L I R Q  
 ggaactgattacaaacattgggccgcaaattgcacaatttgct  
 G T D Y K H W A A N C T I C

### 3'5' Frame 1

aggcaaattgtgcaatttgcgcccaatgtttgtaatcagttccttgtctgattaggtct  
 R Q I V Q F A A Q C L - S V P C L I R S  
 tgggtccccgaaatttccttgggtttgttctggaccacgtctcccaaatgcttgagtgcg  
 W S P K F P W V C S G P R L P N A - V T  
 ttgtactgttttgtggcagtagctttttggcgaggcttttttagatgcctcagcagcagat  
 L Y C F V A V R F W R G F L D A S A A D  
 ttcttagtgacagtttggccttgttgttgttggcctttaccagaaactttgctctcaagc  
 F L V T V W P C C C W P L P E T L L S S  
 tggttcaatctgtctagcagcaatagcgcgagggcagtttcaccacctccgctagccatt

W F N L S S S N S A R A V S P P P L A I  
 cgagcaggagaatttcccctactgctgccaggagttgaatttcttgaattaccgcgacta  
 R A G E F P L L L P G V E F L E L P R L  
 cgtgatgaggagcgcgagaagaggcttgactgccgcctctgcttccctctgcgtagaagcct  
 R D E E R E E A - L P P L L P S A - K P  
 tttggcaatgttgttccttgaggaagttgtagcacggtggcagcattgttattaggattg  
 F G N V V P - G S C S T V A A L L L G L  
 cgggtgccaatgtggtctttgggtgtattcaaggctccctcagttgcaaccatacga  
 R V P M W S L G V F K A P S V A T H T M  
 ccttctttgttagcgccgtagggaagtgaagcttctgggccagttcctaggtaatagaag  
 P S L L A P - G S E A S G P V P R - - K  
 taccatctggggctgagctctttcattttgccgtcaccaccacgaactcgctcgggtagct  
 Y H L G L S S F I L P S P P R T R R V A  
 ctctcggtagtagccaatttgggtcatctggaccactattgggtgttgattggaacgccctgg  
 L R - - P I W S S G P L L V L I G T P W  
 cctcgagggaatctaagttcctccttgccatgctgagtgaagctgtgaaccaagacgca  
 P R G N L S S S L P C - V R A V N Q D A  
 atattattgggtaaacccttggggtcggcgctgttttggccttgccccattgcagtcctcc  
 I L L G K P W G R R C F G L A P L Q S S  
 attctgggtattgtcagttgaatctgtgggtccaccaaataatgcggggggcactacg  
 I L V I V S - I C G S T K C N A G G T T  
 ttggtttgattgggggtccattatcagacattttaatttgttcgtttagagaacagatcta  
 L V - L G S I I R H F N L F V - R T D L  
 caagagatcgaggttggttggtctttcctgggtaggtaaaaaccta  
 Q E I E V G W L F L G R - K P

**3'5' Frame 2**

aggcgaattgtgcaatttgcggcccaatgtttgtaatcagttccttgtctgattaggtctt  
 G K L C N L R P N V C N Q F L V - L G L  
 ggtccccgaaatttcccttgggtttgttctggaccacgtctcccaaatagttgagtacgt  
 G P R N F L G F V L D H V S Q M L E - R  
 tgtactgttttgtggcagtagcttttggcgaggcttttttagatgcctcagcagcagatt  
 C T V L W Q Y V F G E A F - M P Q Q Q I  
 tcttagtgacagtttggccttgttgttggcctttaccagaaactttgctctcaagct  
 S - - Q F G L V V V G L Y Q K L C S Q A  
 ggttcaatctgtctagcagcaatagcgcgagggcagtttcaccacctccgctagccattc  
 G S I C L A A I A R G Q F H H L R - P F  
 gagcaggagaatttcccctactgctgccaggagttgaatttcttgaattaccgcgactac  
 E Q E N F P Y C C Q E L N F L N Y R D Y  
 gtgatgaggagcgcgagaagaggcttgactgccgcctctgcttccctctgcgtagaagcctt  
 V M R S E K R L D C R L C F P L R R S L  
 ttggcaatgttgttccttgaggaagttgtagcacggtggcagcattgttattaggattgc  
 L A M L F L E E V V A R W Q H C Y - D C  
 ggggtgccaatgtggtctttgggtgtattcaaggctccctcagttgcaaccatacga  
 G C Q C G L W V Y S R L P Q L Q P I R C  
 cttctttgttagcgccgtagggaagtgaagcttctgggccagttcctaggtaatagaagt



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L L C - R R R E V K L L G Q F L G N R S  
 accatctggggtgagctctttcattttgccgtcaccaccacgaactcgctcgggtagctc  
 T I W G - A L S F C R H H H E L V G - L  
 ttcggtagtagccaatttggtcatctggaccactattggtggtgattggaacgccctggc  
 F G S S Q F G H L D H Y W C - L E R P G  
 ctcgagggaatctaagttcctccttgccatgctgagtgagagctgtgaaccaagacgcaa  
 L E G I - V P P C H A E - E L - T K T Q  
 tattattgggtaaaccttggggtcggcgctgttttggccttgccccattgcagtcctcca  
 Y Y W V N L G V G A V L A L P H C S P P  
 ttctggttattgtcagttgaatctgtgggtccaccaaataatgcggggggcactacgt  
 F W L L S V E S V G P P N V M R G A L R  
 tggtttgattggggtccattatcagacattttaatttggttcgtttagagaacagatctac  
 W F D W G P L S D I L I C S F R E Q I Y  
 aagagatcgagggttggttggtctttcctgggtaggtaaaaaccta  
 K R S R L V G F S W V G K N L

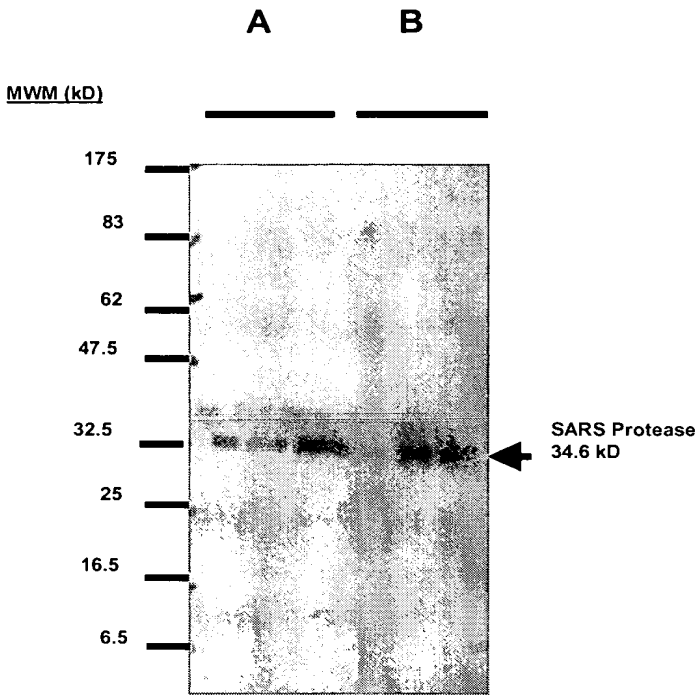
**3'5' Frame 3**

aggcaaattgtgcaatttgcgcccaatgtttgtaatcagttccttgtctgattaggtcttg  
 A N C A I C G P M F V I S S L S D - V L  
 gtccccgaaatttccttgggtttgttctggaccacgtctcccaaatagttgagtgacgtt  
 V P E I S L G L F W T T S P K C L S D V  
 gtactgttttgtggcagtagctttttggcgaggcttttttagatgcctcagcagcagattt  
 V L F C G S T F L A R L F R C L S S R F  
 cttagtgcaggtttggccttgttgttgttggcctttaccagaaactttgctctcaagctg  
 L S D S L A L L L L A F T R N F A L K L  
 gttcaatctgtctagcagcaatagcgcgagggcagtttcaccacctccgctagccattcg  
 V Q S V - Q Q - R E G S F T T S A S H S  
 agcaggagaatttcccctactgctgccaggagttgaatttcttgaattaccgcgactacg  
 S R R I S P T A A R S - I S - I T A T T  
 tgatgaggagcgagaagaggcttgactgccgcctctgcttccctctgcgtagaagccttt  
 - - G A R R G L T A A S A S L C V E A F  
 tggcaatgttggtccttgaggaagttgtagcacggtggcagcattgttattaggattgcg  
 W Q C C S L R K L - H G G S I V I R I A  
 ggtgccaatgtggtctttgggtgtattcaaggtccctcagttgcaaccatacagatgcc  
 G A N V V F G C I Q G S L S C N P Y D A  
 ttctttgttagcgccgtagggaagtgaagcttctgggccaagttccttaggtaatagaagta  
 F F V S A V G K - S F W A S S - V I E V  
 ccactctggggctgagctctttcattttgccgtcaccaccacgaactcgctcgggtagctct  
 P S G A E L F H F A V T T T N S S G S S  
 tcggtagtagccaatttggtcatctggaccactattggtggtgattggaacgccctggcc  
 S V V A N L V I W T T I G V D W N A L A  
 tcgagggaatctaagttcctccttgccatgctgagtgagagctgtgaaccaagacgcaat  
 S R E S K F L L A M L S E S C E P R R N  
 attattgggtaaaccttggggtcggcgctgttttggccttgccccattgcagtcctccat  
 I I G - T L G S A L F W P C P I A V L H  
 tctggttattgtcagttgaatctgtgggtccaccaaataatgcggggggcactacgtt

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S G Y C Q L N L W V H Q M - C G G H Y V  
ggtttgattggggtccattatcagacattttaatttgttcgtttagagaaacagatctaca  
G L I G V H Y Q T F - F V R L E N R S T  
agagatcgaggttggttggttttctgggtaggtaaaaaccta  
R D R G W L A F P G - V K T

**FIGURE 133**



**FIGURE 134**

